HUMAN xiap

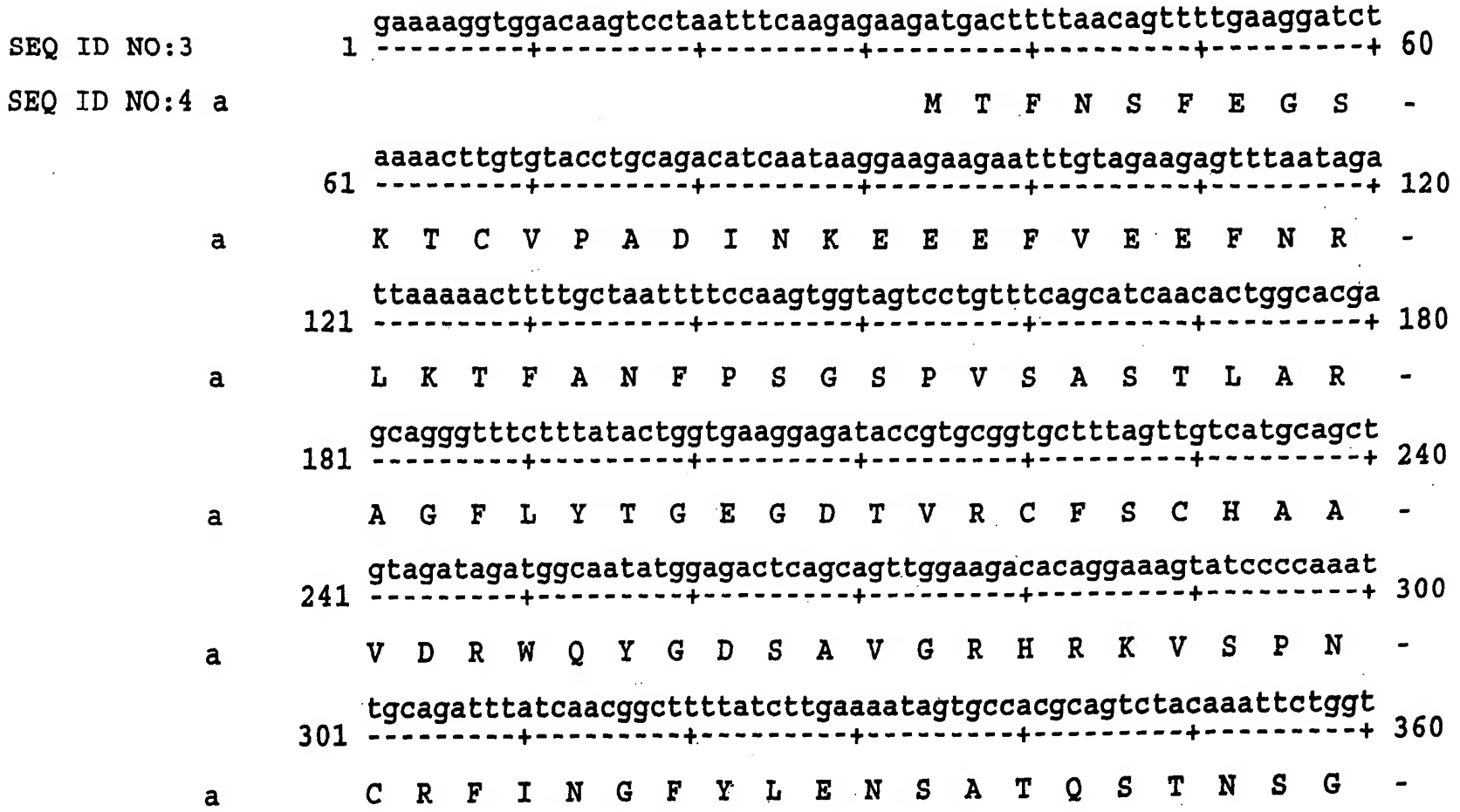

Fig. 1A

HUMAN xiap

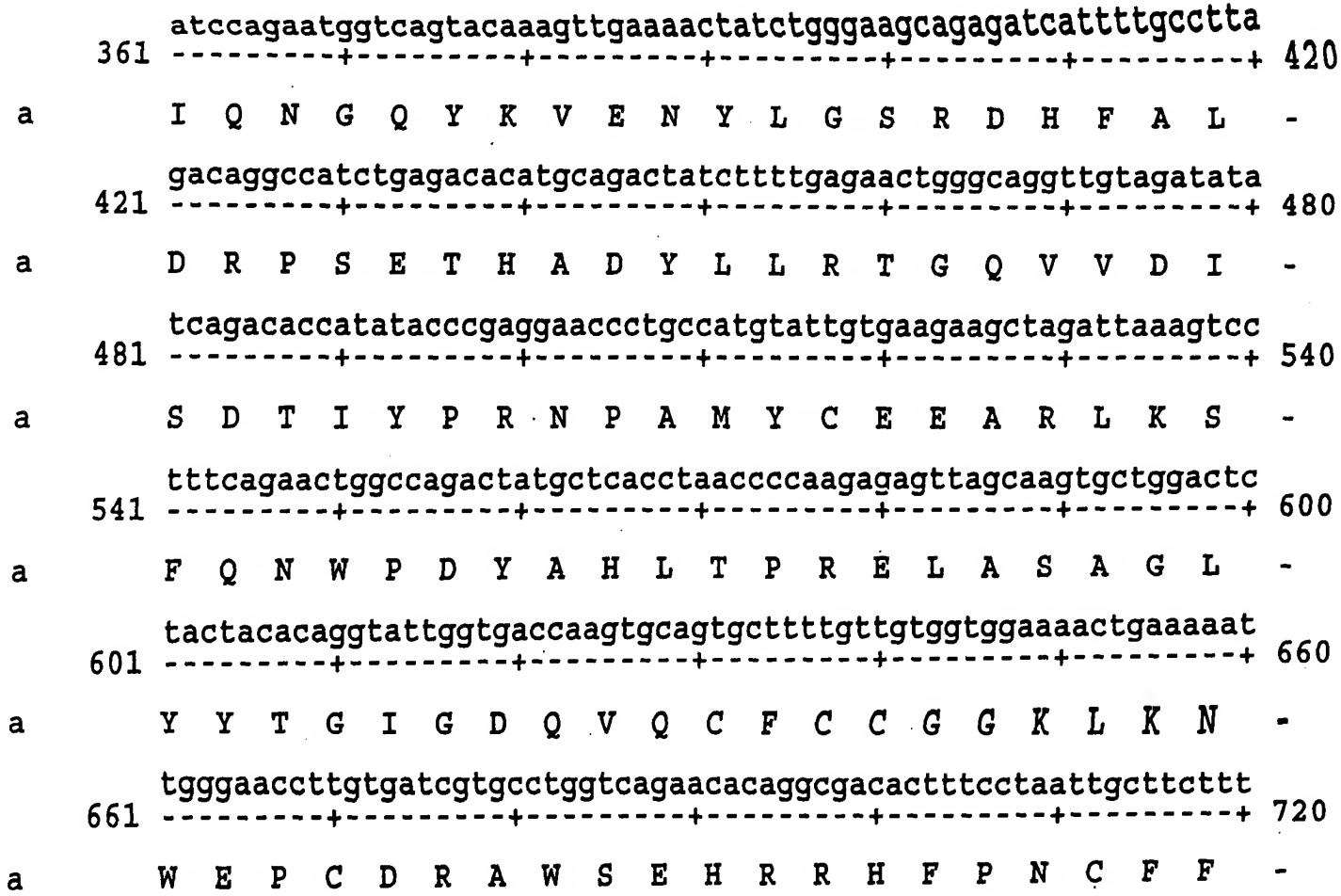

Fig. 1B

HUMAN xiap

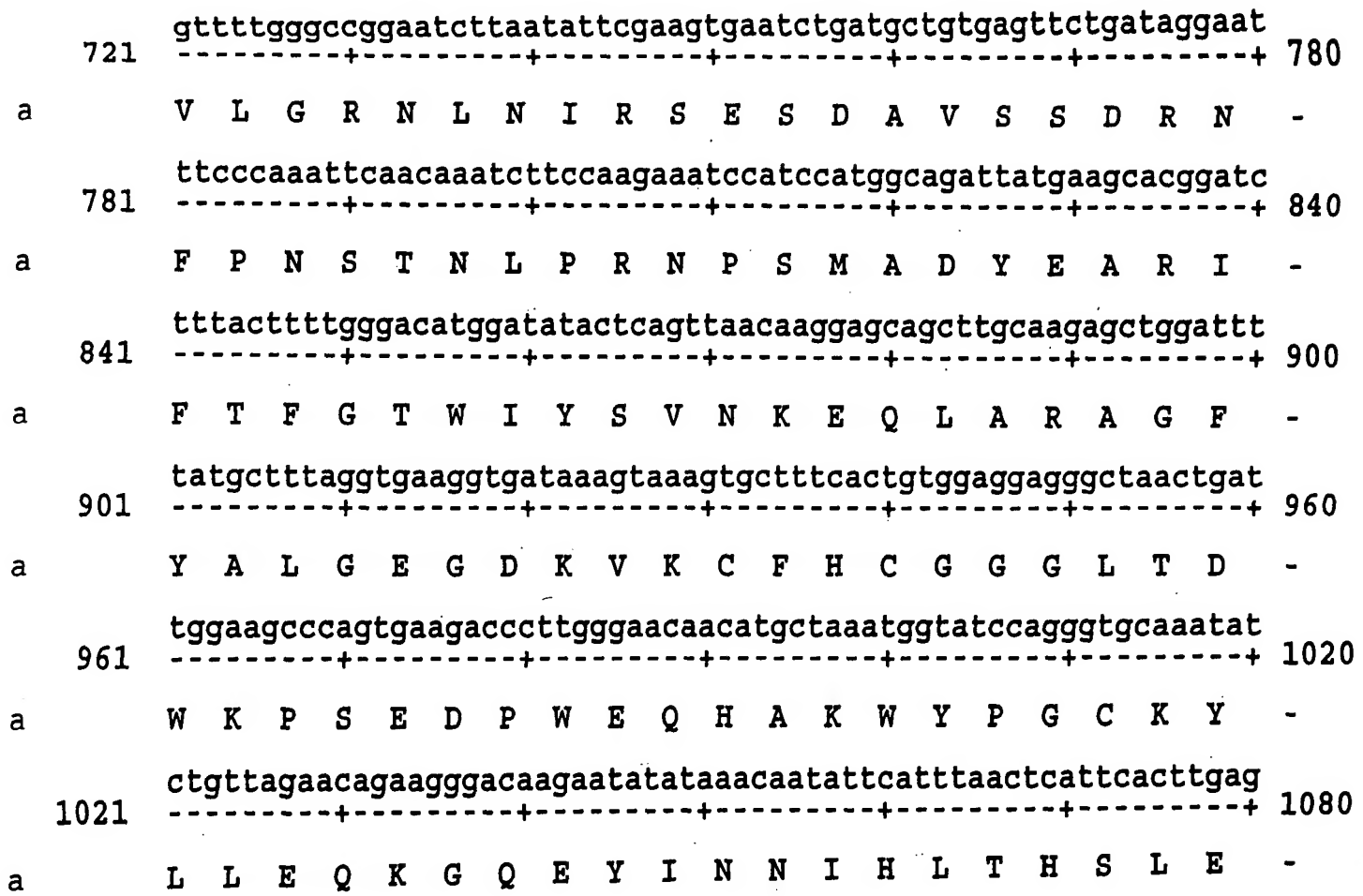

Fig. 1C

HUMAN xiap

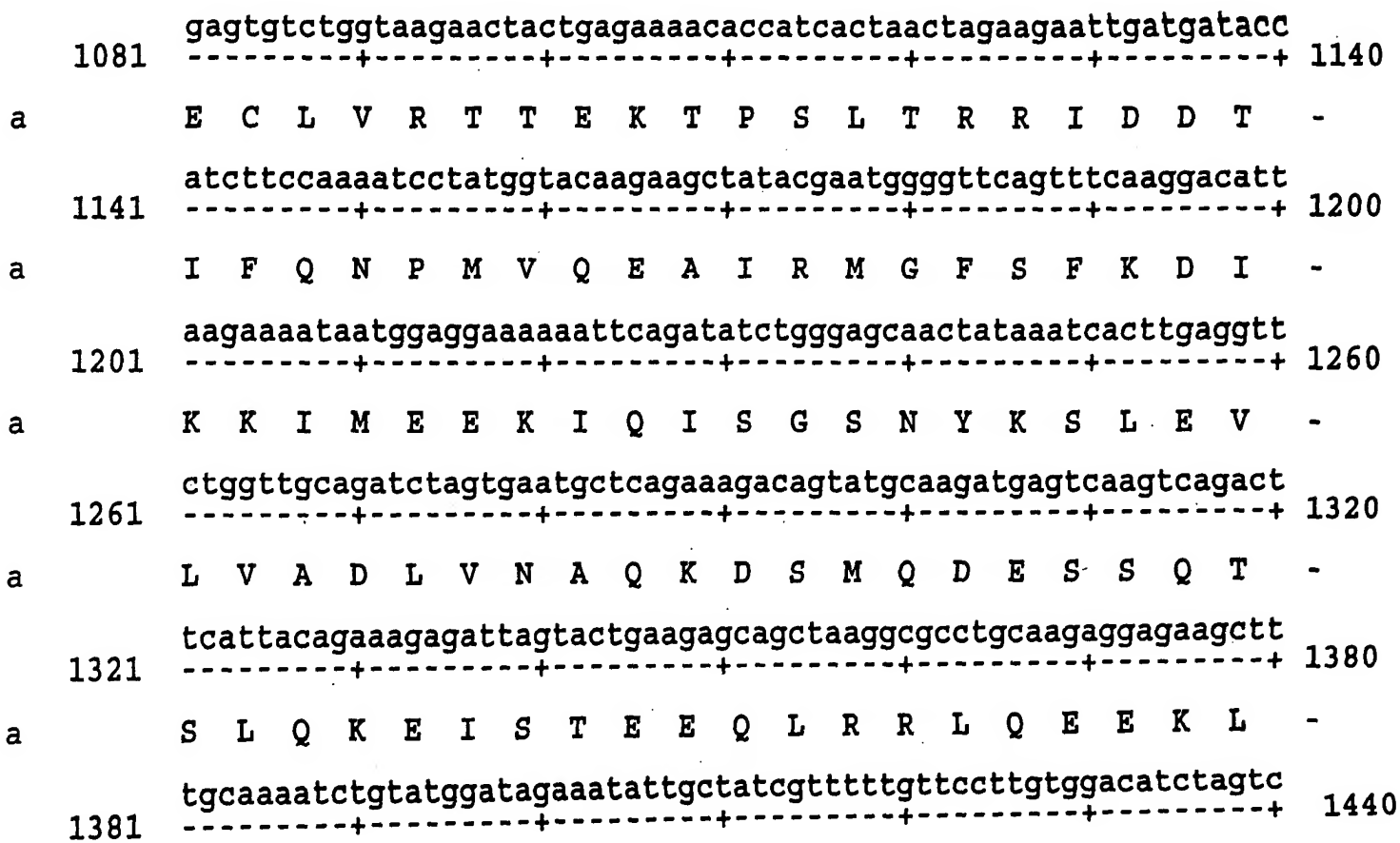

Fig. 1D

HUMAN xiap

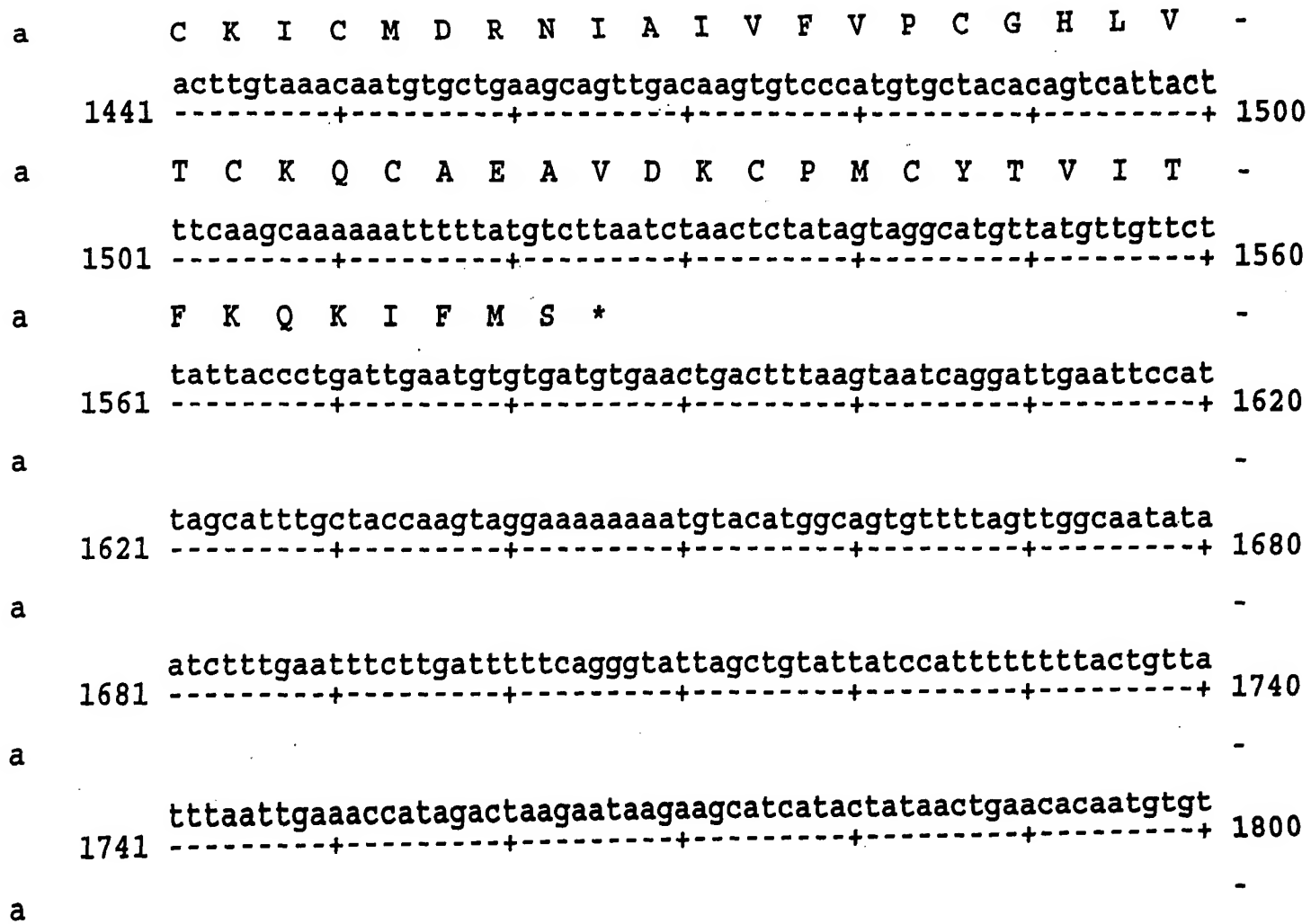

Fig. 1E

HUMAN xiap

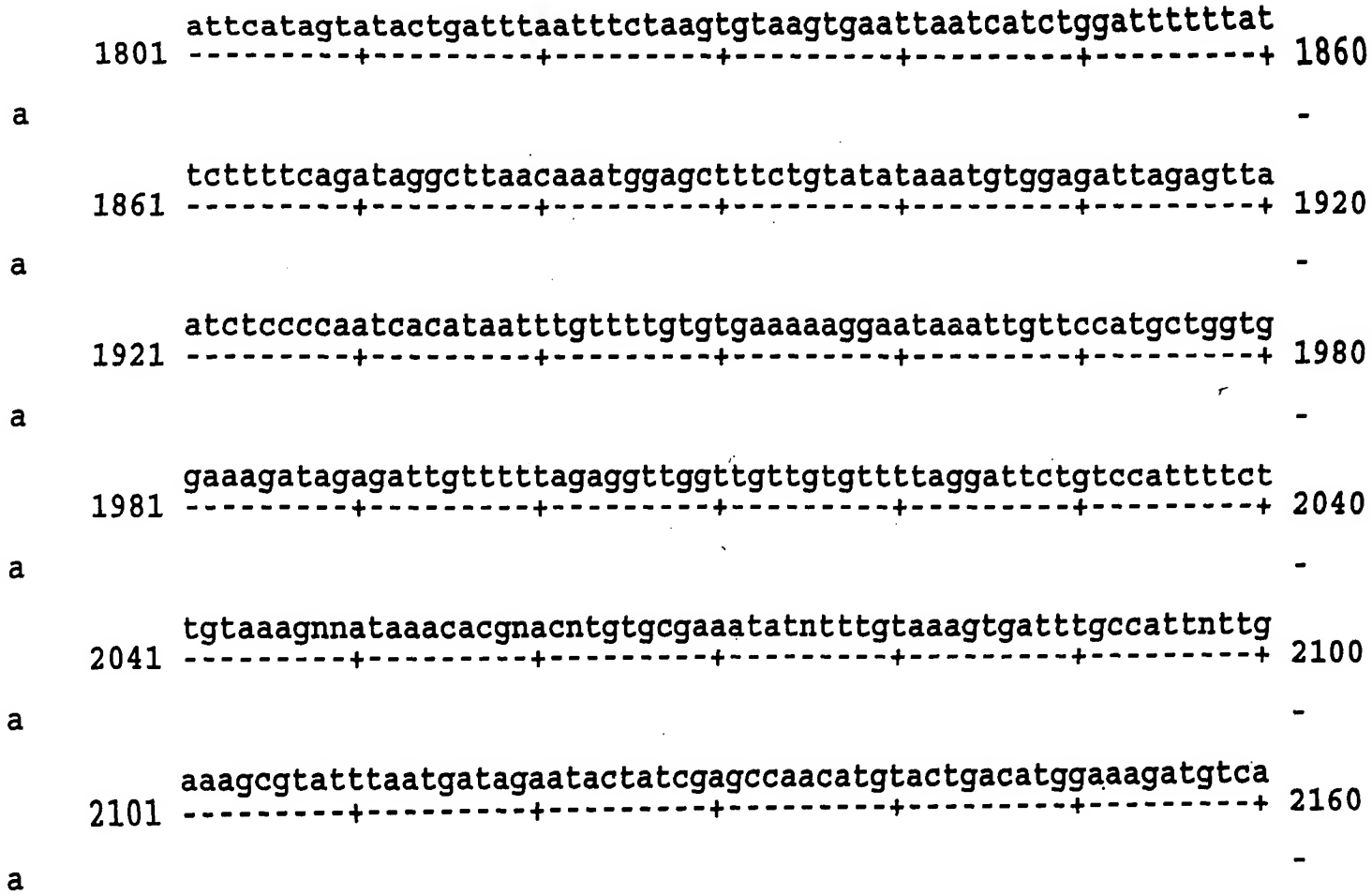

Fig. 1F

HUMAN xiap

```
     nagatatgttaagtgtaaaatgcaagtggcnnnacactatgtatagtctgagccagatca
2161 ---------+---------+---------+---------+---------+---------+ 2220

a                                                                -

     aagtatgtatgttnttaatatgcatagaacnanagatttggaaagatatacaccaaactg
2221 ---------+---------+---------+---------+---------+---------+ 2280

a                                                                -

     ttaaatgtggtttctcttcggggaggggggattgggggaggggccccagaggggtttta
2281 ---------+---------+---------+---------+---------+---------+ 2340

a                                                                -

     naggggccttttcactttcnacttttttcattttgttctgttcgnatttttttataagtat
2341 ---------+---------+---------+---------+---------+---------+ 2400

a                                                                -

     gtanaccccnaagggttttatggnaactaacatcagtaacctaaccccccgtgactatcct
2401 ---------+---------+---------+---------+---------+---------+ 2460

a                                                                -

     gtnctcttcctagggagctgtnttgtttcccacccaccacccttccctctgaacaaatgc
2461 ---------+---------+---------+---------+---------+---------+ 2520

a                                                                -

     ctgagtgctggggcactttn
2521 ---------+---------+ 2540

a                        -
```

Fig. 1G

HUMAN hiap-1

Fig. 2A

HUMAN hiap-1

```
     361 CTGGTGTGAATGACAAGGTCAAATGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAAAA 420
C              G  V  N  D  K  V  K  C  F  C  C  G  L  M  L  D  N  W  K  R  -
     421 GAGGAGACAGTCCTACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCAGATTCGTTCAGA 480
C              G  D  S  P  T  E  K  H  K  K  L  Y  P  S  C  R  F  V  Q  S  -
     481 GTCTAAATTCCGTTAACAACTTGGAAGCTACCTCTCAGCCTACTTTTCCTTCTTCAGTAA 540
C              L  N  S  V  N  N  L  E  A  T  S  Q  P  T  F  P  S  S  V  T  -
     541 CACATTCCACACACTCATTACTTCCGGGTACAGAAAACAGTGGATATTTCCGTGGCTCTT 600
C              H  S  T  H  S  L  L  P  G  T  E  N  S  G  Y  F  R  G  S  Y  -
     601 ATTCAAACTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGAATTTTCTGCCTTGA 660
C              S  N  S  P  S  N  P  V  N  S  R  A  N  Q  E  F  S  A  L  M  -
     661 TGAGAAGTTCCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTACTTACTTTTCAGA 720
C              R  S  S  Y  P  C  P  M  N  N  E  N  A  R  L  L  T  F  Q  T  -
```

Fig. 2B

HUMAN hiap-1

Fig. 2C

HUMAN hiap-1

```
      GACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCAACATGCCAAGTGGTTTCCAA
1081  ---------+---------+---------+---------+---------+---------+ 1140
c          L  R  C  W  E  S  G  D  D  P  W  V  Q  H  A  K  W  F  P  R -

      GGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTCATCCGTCAAGTTCAAGCCAGTT
1141  ---------+---------+---------+---------+---------+---------+ 1200
c          C  E  Y  L  I  R  I  K  G  Q  E  F  I  R  Q  V  Q  A  S  Y -

      ACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCCAGGAGATGAAAATGCAG
1201  ---------+---------+---------+---------+---------+---------+ 1260
c          P  H  L  L  E  Q  L  L  S  T  S  D  S  P  G  D  E  N  A  E -

      AGTCATCAATTATCCATTTGGAACCTGGAGAAGACCATTCAGAAGATGCAATCATGATGA
1261  ---------+---------+---------+---------+---------+---------+ 1320
c          S  S  I  I  H  L  E  P  G  E  D  H  S  E  D  A  I  M  M  N -

      ATACTCCTGTGATTAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCCTGGTAAAACAGA
1321  ---------+---------+---------+---------+---------+---------+ 1380
c          T  P  V  I  N  A  A  V  E  M  G  F  S  R  S  L  V  K  Q  T -

      CAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAATTATAGACTAGTCAATGATCTTGTGT
1381  ---------+---------+---------+---------+---------+---------+ 1440
c          V  Q  R  K  I  L  A  T  G  E  N  Y  R  L  V  N  D  L  V  L -
```

Fig. 2D

HUMAN hiap-1

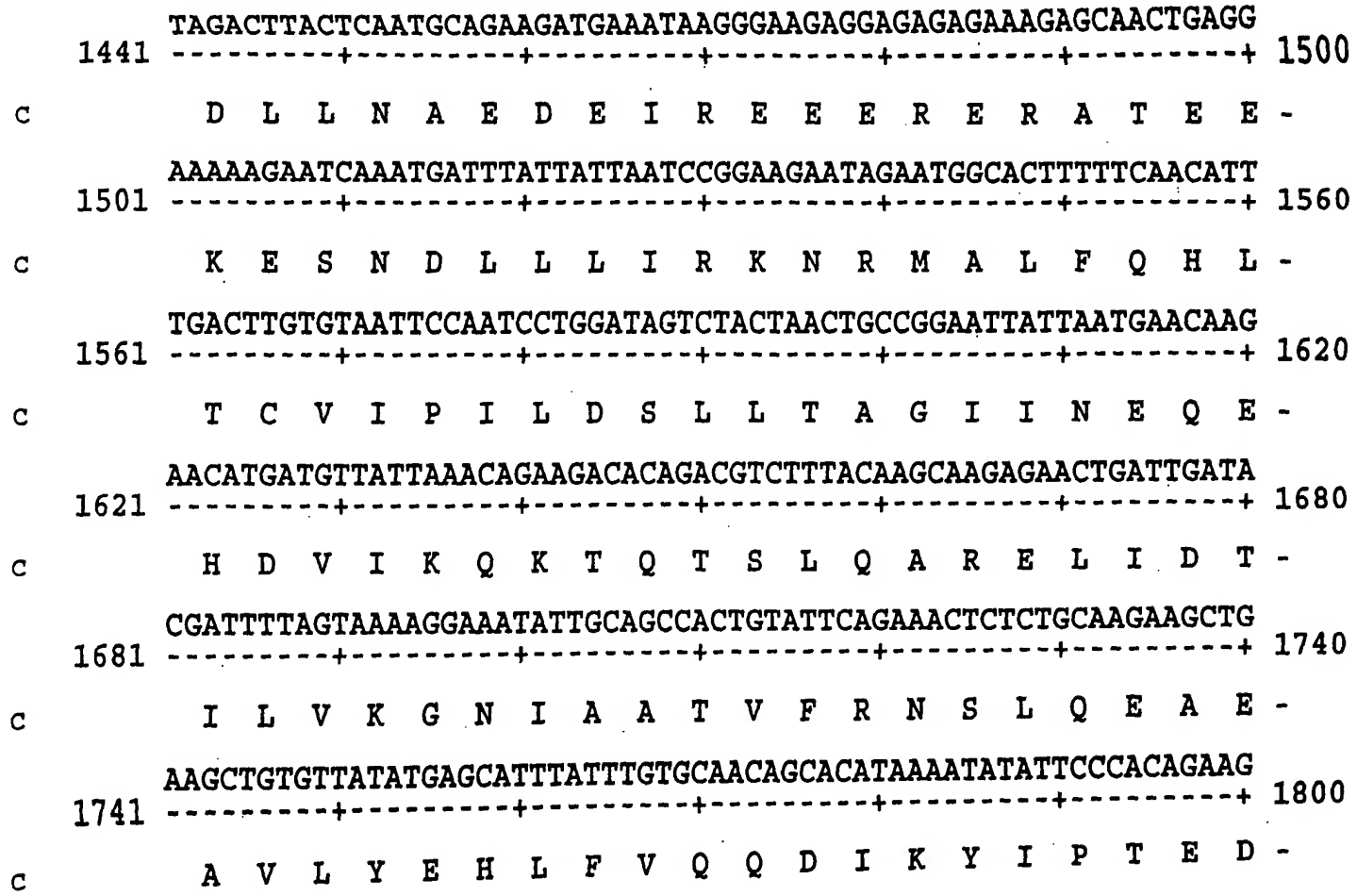

Fig. 2E

HUMAN hiap-1

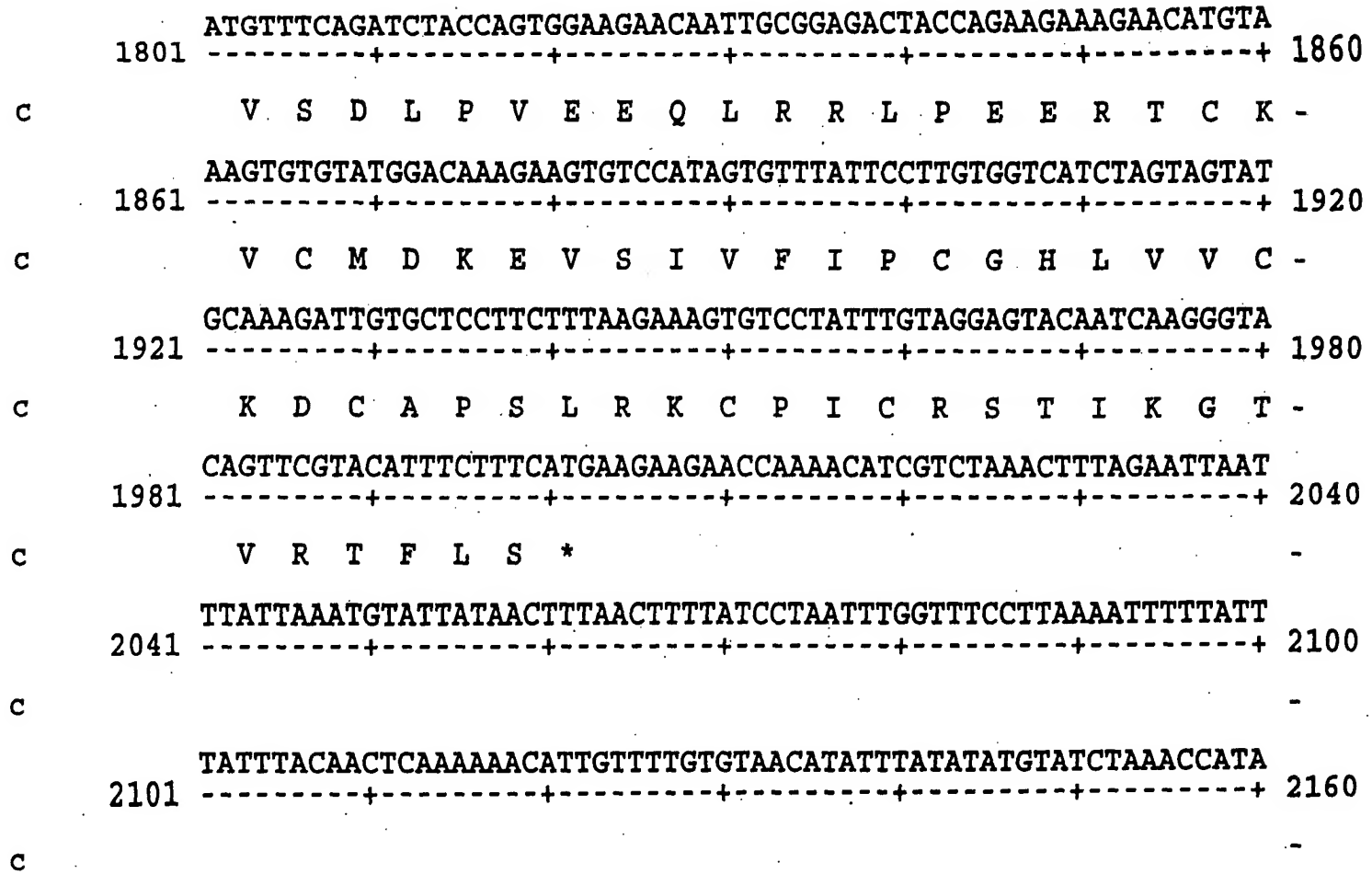

Fig. 2F

HUMAN hiap-1

Fig. 2G

HUMAN hiap-1

```
     CAGTGTCCTATACATCGAAGGTGTGCATATATGTTGAATCACATTTTAGGGACATGGTGT
2521 ---------+---------+---------+---------+---------+---------+ 2580

c                                                                -

     TTTTATAAAGAATTCTGTGAGXAAAAATTTAATAAAGCAACCXAAATTACTCTTAAAAAA
2581 ---------+---------+---------+---------+---------+---------+ 2640

c                                                                -

     AAAAAAAAAAAAAAAACTCGAGGGGCCCGTACCAAT
2641 ---------+---------+---------+------ 2676

c                                        -
```

Fig. 2H

HUMAN hiap-2

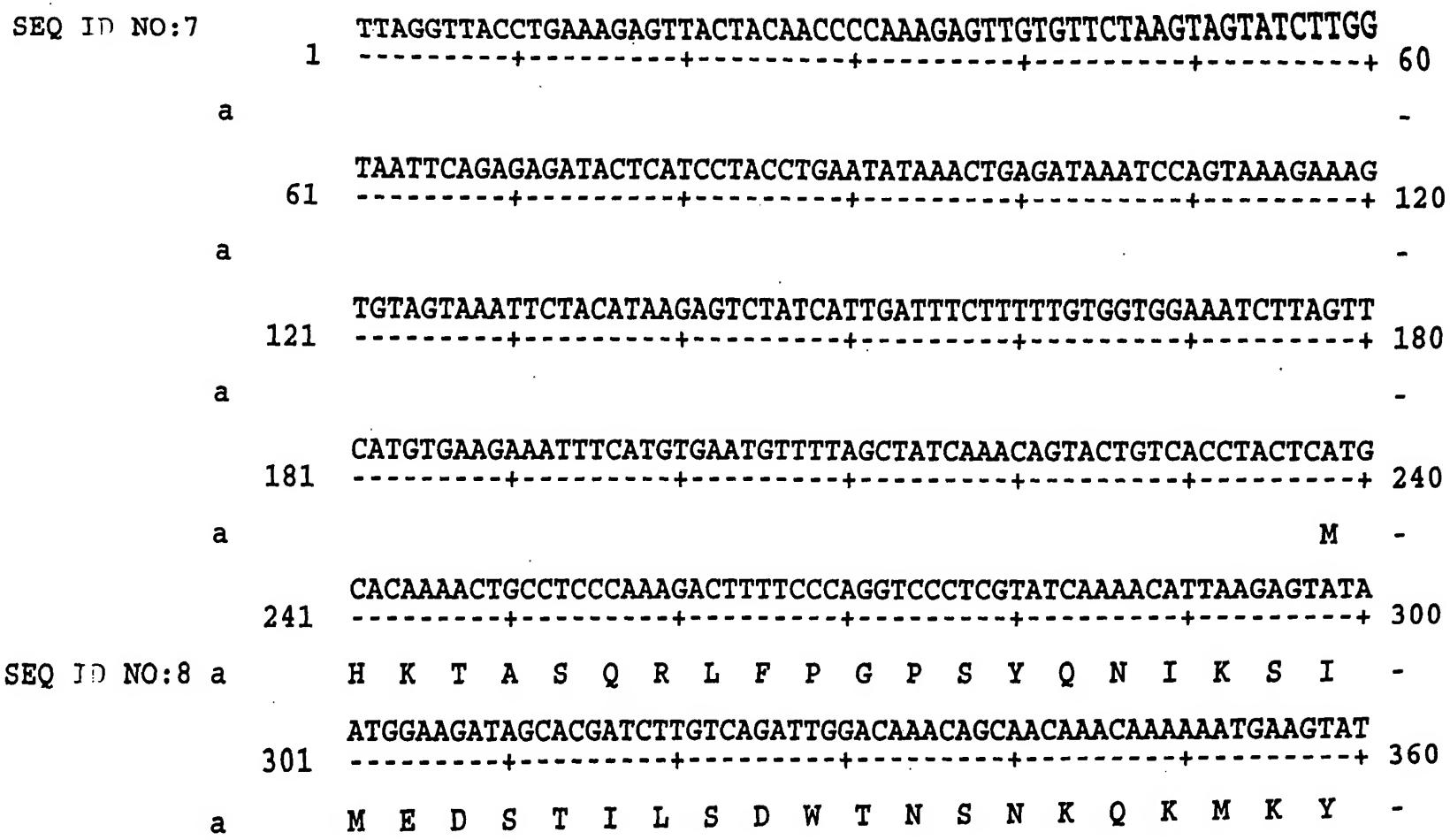

Fig. 3A

HUMAN hiap-2

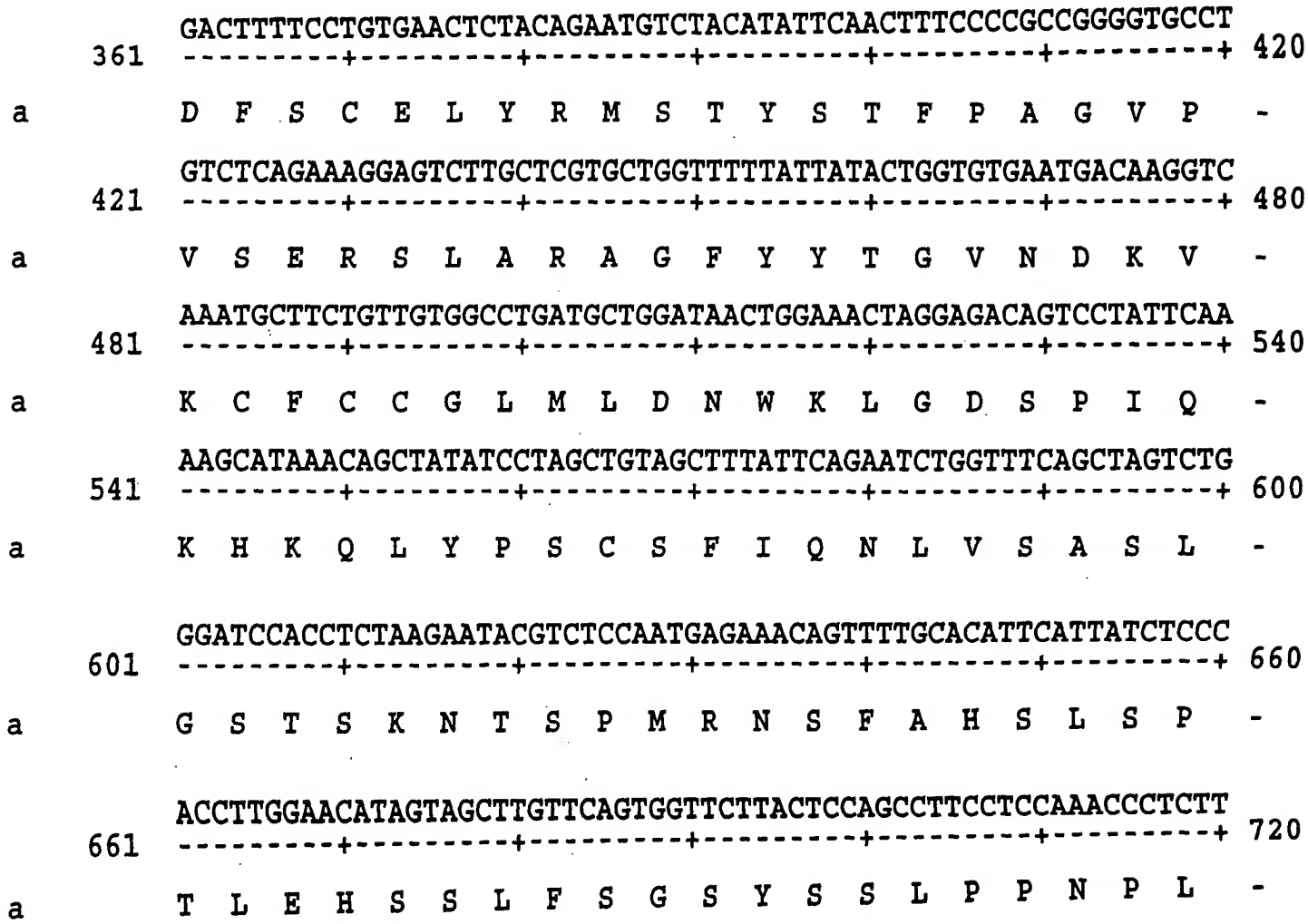

Fig. 3B

HUMAN hiap-2

Fig. 3C

HUMAN hiap-2

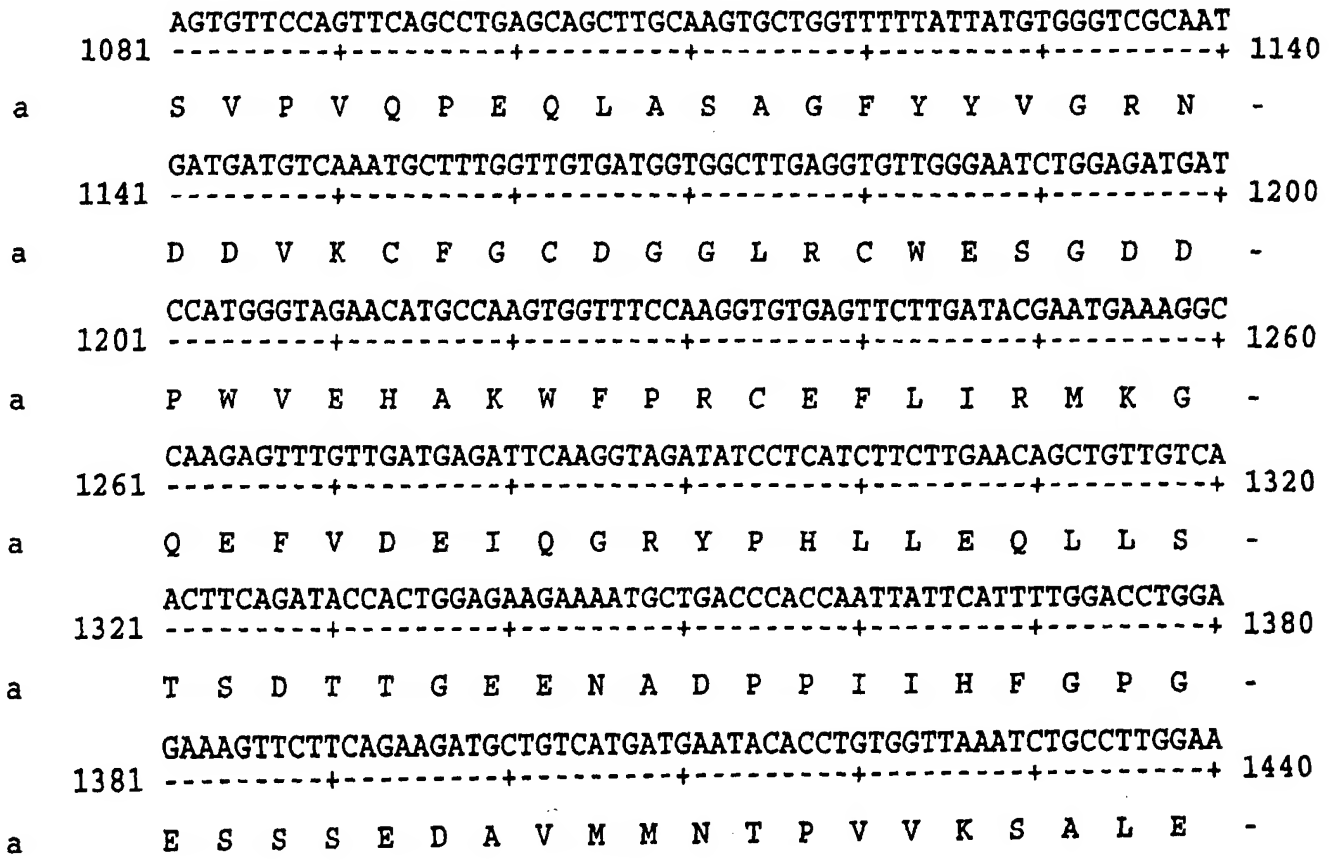

Fig. 3D

HUMAN hiap-2

Fig. 3E

HUMAN hiap-2

Fig. 3F

HUMAN hiap-2

Fig. 3G

MOUSE xiap

Fig. 4A

MOUSE xiap

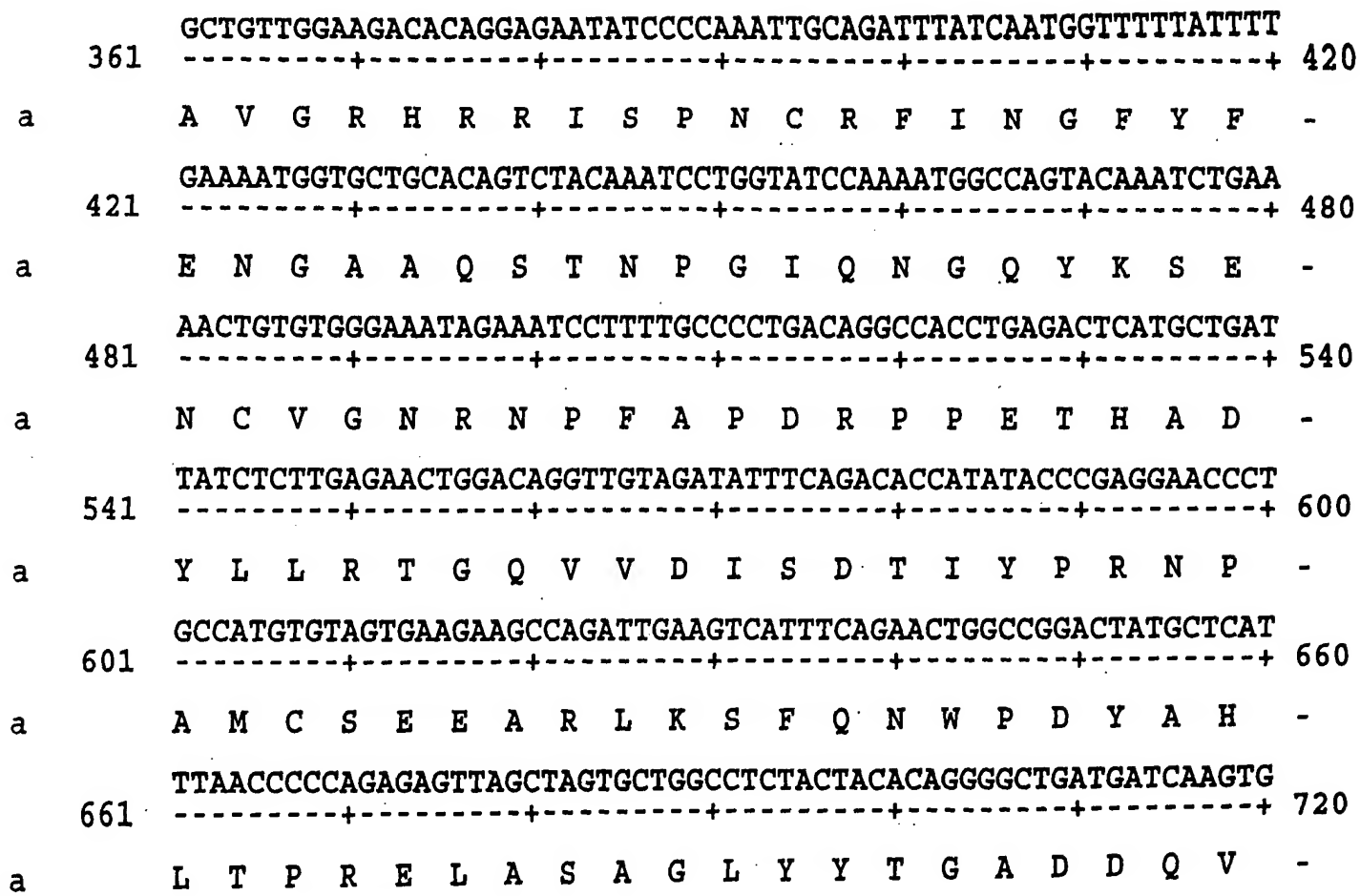

Fig. 4B

MOUSE xiap

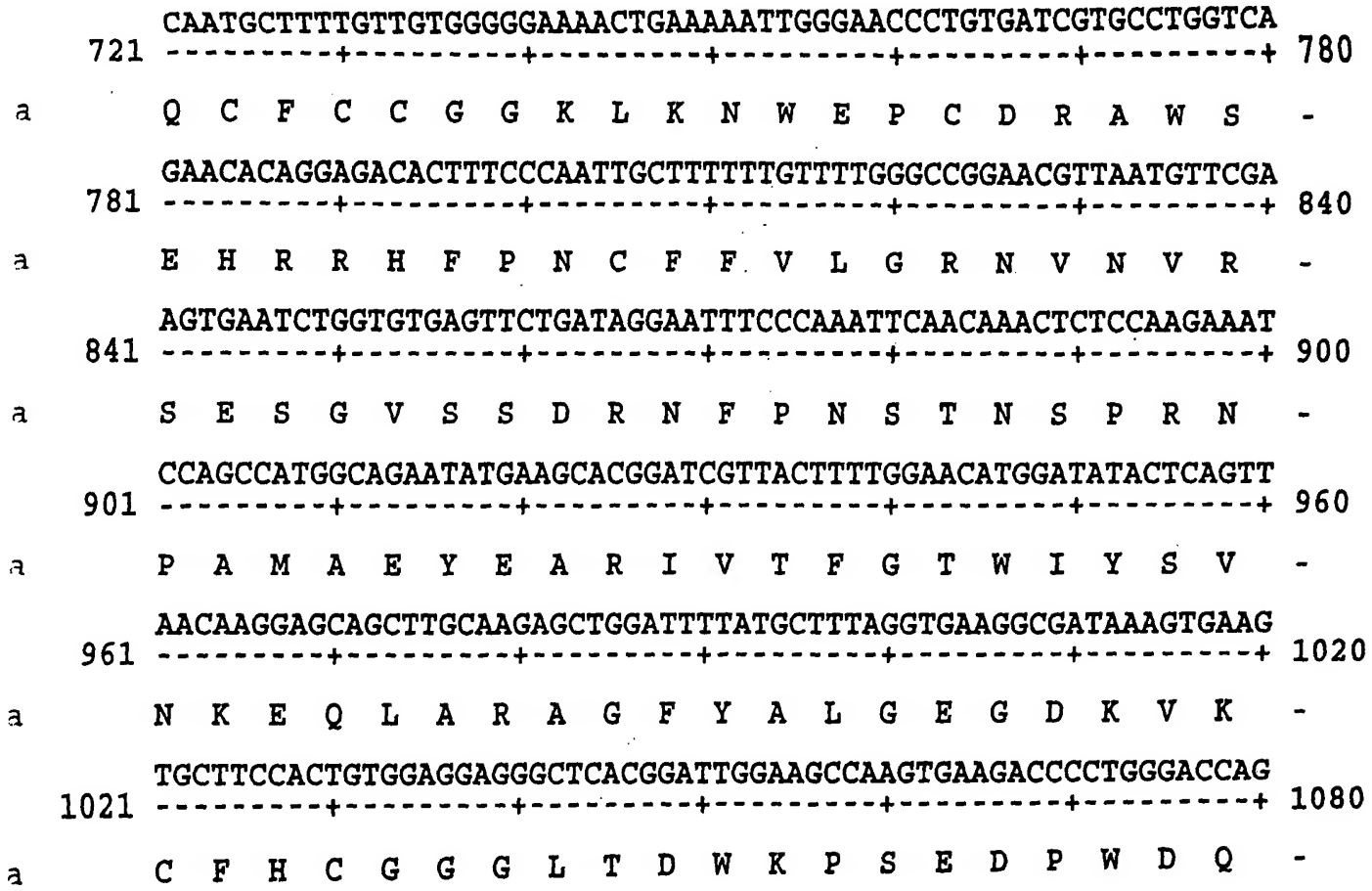

Fig. 4C

MOUSE xiap

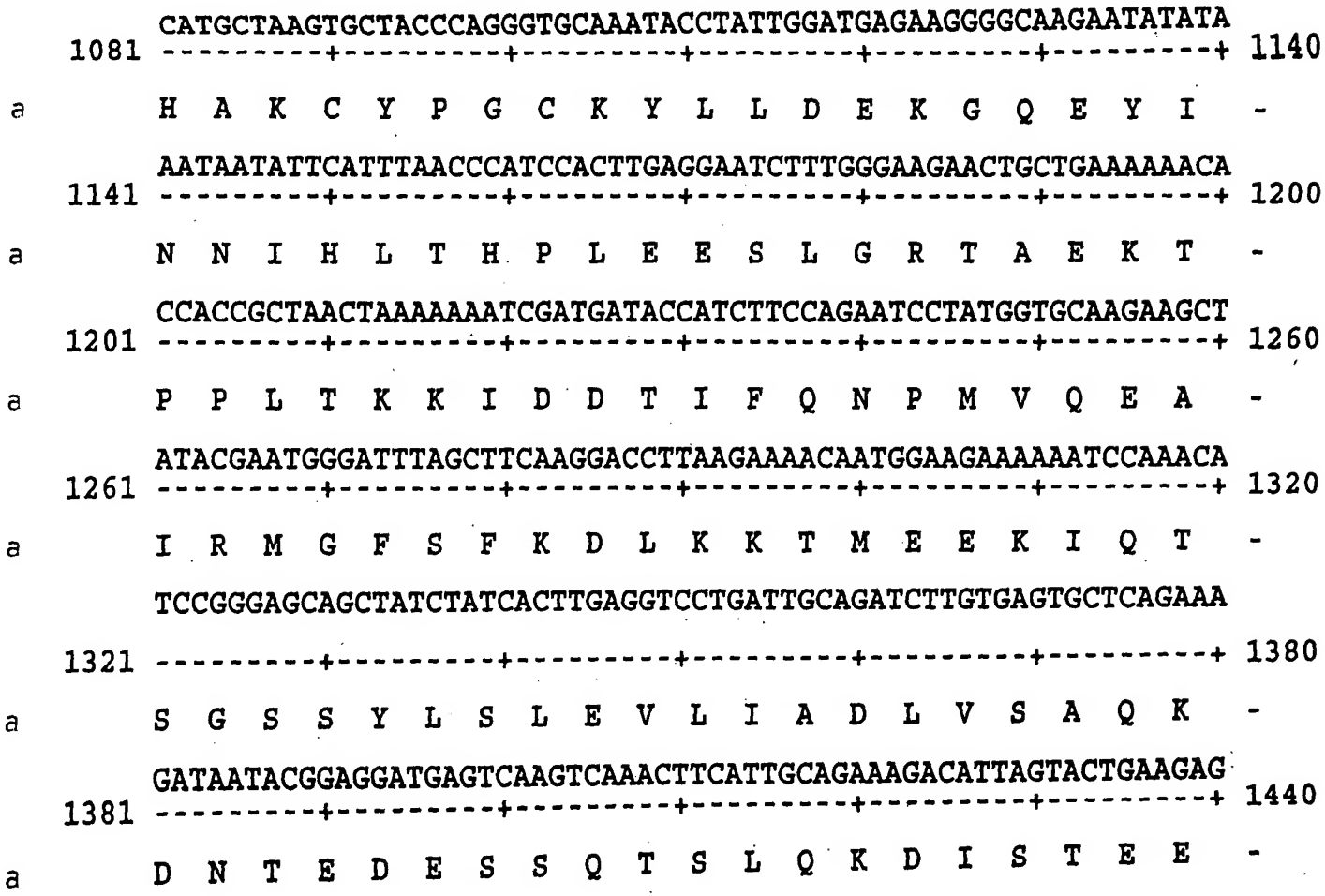

Fig. 4D

MOUSE xiap

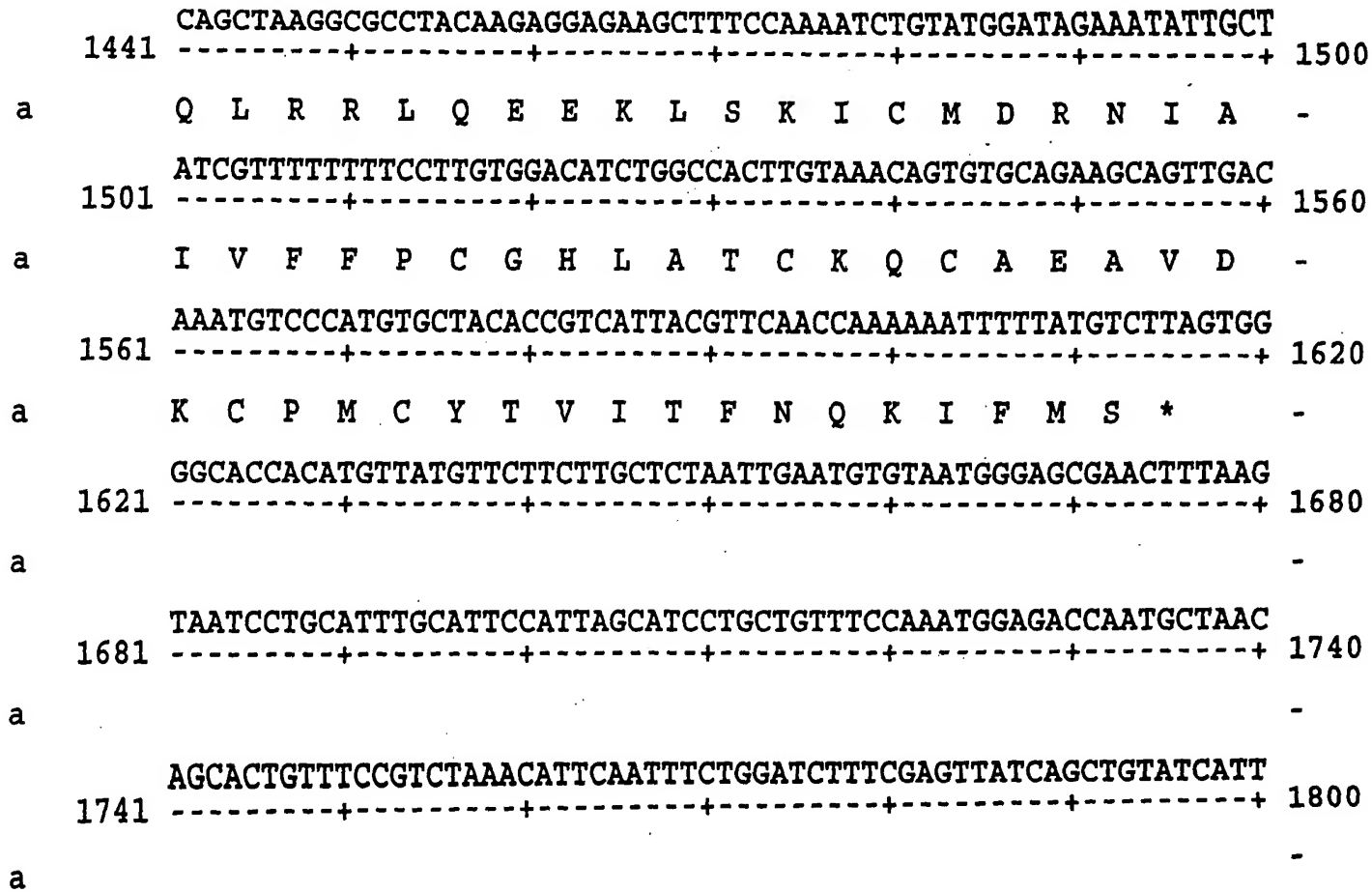

Fig. 4E

MOUSE xiap

```
     TAGCCAGTGTTTTACTCGATTGAAACCTTAGACAGAGAAGCATTTTATAGCTTTTCACAT
1801 ---------+---------+---------+---------+---------+---------+ 1860
a                                                                -

     GTATATTGGTAGTACACTGACTTGATTTCTATATGTAAGTGAATTCATCACCTGCATGTT
1861 ---------+---------+---------+---------+---------+---------+ 1920
a                                                                -

     TCATGCCTTTTGCATAAGCTTAACAAATGGAGTGTTCTGTATAAGCATGGAGATGTGATG
1921 ---------+---------+---------+---------+---------+---------+ 1980
a                                                                -

     GAATCTGCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAAGAACTGCCCCACGCTG
1981 ---------+---------+---------+---------+---------+---------+ 2040
a                                                                -

     CTGGGAGGATAAAGATTGTTTTAGATGCTCACTTCTGTGTTTTAGGATTCTGCCCATTTA
2041 ---------+---------+---------+---------+---------+---------+ 2100
```

Fig. 4F

M-hiap-1

Fig. 5A

M-hiap-1

```
    CACAGAAAGTTGTACCCCAGCTGCAACTTTGTACAGACTTTGAATCCAGCCAACAGTCTG
421 ---------+---------+---------+---------+---------+---------+ 480
    H  R  K  L  Y  P  S  C  N  F  V  Q  T  L  N  P  A  N  S  L   -

    GAAGCTAGTCCTCGGCCTTCTCTTCCTTCCACGGCGATGAGCACCATGCCTTTGAGCTTT
481 ---------+---------+---------+---------+---------+---------+ 540
    E  A  S  P  R  P  S  L  P  S  T  A  M  S  T  M  P  L  S  F   -

    GCAAGTTCTGAGAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTTCCCTCAGACCCT
541 ---------+---------+---------+---------+---------+---------+ 600
    A  S  S  E  N  T  G  Y  F  S  G  S  Y  S  S  F  P  S  D  P   -

    GTGAACTTCCGAGCAAATCAAGATTGTCCTGCTTTGAGCACAAGTCCCTACCACTTTGCA
601 ---------+---------+---------+---------+---------+---------+ 660
    V  N  F  R  A  N  Q  D  C  P  A  L  S  T  S  P  Y  H  F  A   -

    ATGAACACAGAGAAGGCCAGATTACTCACCTATGAAACATGGCCATTGTCTTTTCTGTCA
661 ---------+---------+---------+---------+---------+---------+ 720
    M  N  T  E  K  A  R  L  L  T  Y  E  T  W  P  L  S  F  L  S   -

    CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGGACCTGGAGATAGAGTGGCCTGC
721 ---------+---------+---------+---------+---------+---------+ 780
    P  A  K  L  A  K  A  G  F  Y  Y  I  G  P  G  D  R  V  A  C   -
```

Fig. 5B

M-hiap-1

```
    TTTGCGTGCGATGGGAAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC
781 ---------+---------+---------+---------+---------+---------+ 840
    F  A  C  D  G  K  L  S  N  W  E  R  K  D  D  A  M  S  E  H   -

    CAGAGGCATTTCCCCAGCTGTCCGTTCTTALLkGACTTGGGTCAGTCTGCTTCGAGATAC
841 ---------+---------+---------+---------+---------+---------+ 900
    Q  R  H  F  P  S  C  P  F  L  K  D  L  G  Q  S  A  S  R  Y   -

    ACTGTCTCTAACCTGAGCATGCAGACACACGCAGCCCGTATTAGAACATTCTCTAACTGG
901 ---------+---------+---------+---------+---------+---------+ 960
    T  V  S  N  L  S  M  Q  T  H  A  A  R  I  R  T  F  S  N  W   -

    CCTTCTAGTGCACTAGTTCATTCCCAGGAACTTGCAAGTGCGGGCTTTTATTATACAGGA
961 ---------+---------+---------+---------+---------+---------+ 1020
    P  S  S  A  L  V  H  S  Q  E  L  A  S  A  G  F  Y  Y  T  G   -

    CACAGTGATGATGTCAAGTGTTTATGCTGTGATGGTGGGCTGAGGTGCTGGGAATCTGGA
1021 ---------+---------+---------+---------+---------+---------+ 1080
    H  S  D  D  V  K  C  L  C  C  D  G  G  L  R  C  W  E  S  G   -

    GATGACCCCTGGGTGGAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTTGCTCAGAATC
1081 ---------+---------+---------+---------+---------+---------+ 1140
    D  D  P  W  V  E  H  A  K  W  F  P  R  C  E  Y  L  L  R  I   -

    AAAGGCCAAGAATTTGTCAGCCAAGTTCAAGCTGGCTATCCTCATCTACTTGAGCAGCTA
1141 ---------+---------+---------+---------+---------+---------+ 1200
    K  G  Q  E  F  V  S  Q  V  Q  A  G  Y  P  H  L  L  E  Q  L   -
```

Fig. 5C

M-hiap-1

Fig. 5D

M-hiap-1

```
     TGCCTCCTAAGTGCAAGGGCCATCACTGAACAGGAGTGCAATGCTGTGAAACAGAAACCA
1561 ---------+---------+---------+---------+---------+---------+ 1620
     C  L  L  S  A  R  A  I  T  E  Q  E  C  N  A  V  K  Q  K  P   -

     CACACCTTACAAGCAAGCACACTGATTGATACTGTGTTAGCAAAAGGAAACACTGCAGCA
1621 ---------+---------+---------+---------+---------+---------+ 1680
     H  T  L  Q  A  S  T  L  I  D  T  V  L  A  K  G  N  T  A  A   -

     ACCTCATTCAGAAACTCCCTTCGGGAAATTGACCCTGCGTTATACAGAGATATATTTGTG
1681 ---------+---------+---------+---------+---------+---------+ 1740
     T  S  F  R  N  S  L  R  E  I  D  P  A  L  Y  R  D  I  F  V   -

     CAACAGGACATTAGGAGTCTTCCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG
1741 ---------+---------+---------+---------+---------+---------+ 1800
     Q  Q  D  I  R  S  L  P  T  D  D  I  A  A  L  P  M  E  E  Q   -

     TTGCGGCCCCTCCCGGAGGACAGAATGTGTAAAGTGTGTATGGACCGAGAGGTATCCATC
1801 ---------+---------+---------+---------+---------+---------+ 1860
     L  R  P  L  P  E  D  R  M  C  K  V  C  M  D  R  E  V  S  I   -

     GTGTTCATTCCCTGTGGCCATCTGGTCGTGTGCAAAGACTGCGCTCCCTCTCTGAGGAAG
1861 ---------+---------+---------+---------+---------+---------+ 1920
     V  F  I  P  C  G  H  L  V  V  C  K  D  C  A  P  S  L  R  K   -
```

Fig. 5E

M-hiap-1

```
     TGTCCCATCTGTAGAGGGACCATCAAGGGCACAGTGCGCACATTTCTCTCCTGAACAAGA
1921 ---------+---------+---------+---------+---------+---------+ 1980
     C  P  I  C  R  G  T  I  K  G  T  V  R  T  F  L  S  *         -

     CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACTGTCACTCCCAGTTCCAT
1981 ---------+---------+---------+---------+---------+---------+ 2040
     TCGGAACTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACkCACAAATATAAACAT
2041 ---------+---------+---------+---------+---------+---------+ 2100
     GAAAAACTTTTGTCTGAAGTCAAGAATGAATGAATTACTTATATAATAATTTTAATTGGT
2101 ---------+---------+---------+---------+---------+---------+ 2160
     TTCCTTAAAAGTGCTATTTGTTCCCAACTCAGAAAATTGTTTTCTGTAAACATATTTACA
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TACTACCTGCATCTAAAGTATTCATATATTCATATATTCAGATGTCATGAGAGAGGGTTT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TGTTCTTGTTCCTGAAAAGCTGGTTTATCATCTGATCAGCATATACTGCGCAACGGGCAG
2281 ---------+---------+---------+---------+---------+---------+ 2340
     GGCTAGAATCCATGAACCAAGCTGCAAAGATCTCACGCTAAATAAGGCGGAAAGATTTGG
2341 ---------+---------+---------+---------+---------+---------+ 2400
     AGAAACGAAAGGAAATTCTTTCCTGTCCAATGTATACTCTTCAGACTAATGACCTCTTCC
2401 ---------+---------+---------+---------+---------+---------+ 2460
     TATCAAGCCTTCTA
2461 ---------+---- 2474
```

Fig. 5F

M-hiap-2

Fig. 6A

M-hiap-2

```
    GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAATATGTCTCCTGTGAAAAGTAG
421 ---------+---------+---------+---------+---------+---------+ 480
     T  L  L  S  A  S  L  Q  S  P  S  K  N  M  S  P  V  K  S  R  -

    ATTTGCACATTCGTCACCTCTGGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC
481 ---------+---------+---------+---------+---------+---------+ 540
     F  A  H  S  S  P  L  E  R  G  G  I  H  S  N  L  C  S  S  P  -

    TCTTAATTCTAGAGCAGTGGAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
541 ---------+---------+---------+---------+---------+---------+ 600
     L  N  S  R  A  V  E  D  F  S  S  R  M  D  P  C  S  Y  A  M  -

    GAGTACAGAAGAGGCCAGATTTCTTACTTACAGTATGTGGCCTTTAAGTTTTCTGTCACC
601 ---------+---------+---------+---------+---------+---------+ 660
     S  T  E  E  A  R  F  L  T  Y  S  M  W  P  L  S  F  L  S  P  -

    AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGGCCTGGAGACAGGGTGGCCTGTTT
661 ---------+---------+---------+---------+---------+---------+ 720
     A  E  L  A  R  A  G  F  Y  Y  I  G  P  G  D  R  V  A  C  F  -

    TGCCTGTGGTGGGAAACTGAGCAACTGGGAACCAAAGGATTATGCTATGTCAGAGCACCG
721 ---------+---------+---------+---------+---------+---------+ 780
     A  C  G  G  K  L  S  N  W  E  P  K  D  Y  A  M  S  E  H  R  -
```

Fig. 6B

M-hiap-2

```
    CAGACATTTTCCCCACTGTCCATTTCTGGAAAATACTTCAGAAACACAGAGGTTTAGTAT
781 ---------+---------+---------+---------+---------+---------+ 840
     R  H  F  P  H  C  P  F  L  E  N  T  S  E  T  Q  R  F  S  I  -

    ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACC
841 ---------+---------+---------+---------+---------+---------+ 900
     S  N  L  S  M  Q  T  H  S  A  R  L  R  T  F  L  Y  W  P  P  -

    TAGTGTTCCTGTTCAGCCCGAGCAGCTTGCAAGTGCTGGATTCTATTACGTGGATCGCRA
901 ---------+---------+---------+---------+---------+---------+ 960
     S  V  P  V  Q  P  E  Q  L  A  S  A  G  F  Y  Y  V  D  R  N  -

    TGATGATGTCAAGTGCCTTTGTTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGA
961 ---------+---------+---------+---------+---------+---------+ 1020
     D  D  V  K  C  L  C  C  D  G  G  L  R  C  W  E  P  G  D  D  -

    CCCCTGGATAGAACACGCCAAATGGTTTCCAAGGTGTGAGTTCTTGATACGGATGAAGGG
1021 ---------+---------+---------+---------+---------+---------+ 1080
     P  W  I  E  H  A  K  W  F  P  R  C  E  F  L  I  R  M  K  G  -

    TCAGGAGTTTGTTGATGAGATTCAAGCTAGATATCCTCATCTTCTTGAGCAGCTGTTGTC
1081 ---------+---------+---------+---------+---------+---------+ 1140
     Q  E  F  V  D  E  I  Q  A  R  Y  P  H  L  L  E  Q  L  L  S  -
```

Fig. 6C

M-hiap-2

Fig. 6D

M-hiap-2

```
     TAATCTTCTTGAGGCCAGTGTAATTACAAAACAGGAACATGATATTATTAGACAGAAAAC
1501 ---------+---------+---------+---------+---------+---------+ 1560
      N  L  L  E  A  S  V  I  T  K  Q  E  H  D  I  I  R  Q  K  T  -

     ACAGATACCCTTACAAGCAAGAGAGCTTATTGACACCGTTTTAGTCAAGGGAAATGCTGC
1561 ---------+---------+---------+---------+---------+---------+ 1620
      Q  I  P  L  Q  A  R  E  L  I  D  T  V  L  V  K  G  N  A  A  -

     AGCCAACATCTTCAAAAACTCTCTGAAGGGAATTGACTCCACGTTATATGAAAACTTATT
1621 ---------+---------+---------+---------+---------+---------+ 1680
      A  N  I  F  K  N  S  L  K  G  I  D  S  T  L  Y  E  N  L  F  -

     TGTGGAAAAGAATATGAAGTATATTCCAACAGAAGACGTTTCAGGCTTGTCATTGGAAGA
1681 ---------+---------+---------+---------+---------+---------+ 1740
      V  E  K  N  M  K  Y  I  P  T  E  D  V  S  G  L  S  L  E  E  -

     GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAAGTGTGTATGGACAGAGAGGTTTC
1741 ---------+---------+---------+---------+---------+---------+ 1800
      Q  L  R  R  L  Q  E  E  R  T  C  K  V  C  M  D  R  E  V  S  -

     TATTGTGTTCATTCCGTGTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCCTTCTCTAAG
1801 ---------+---------+---------+---------+---------+---------+ 1860
      I  V  F  I  P  C  G  H  L  V  V  C  Q  E  C  A  P  S  L  R  -
```

Fig. 6E

M-hiap-2

```
     GAAGTGCCCCATCTGCAGGGGGACAATCAAGGGGACTGTGCGCACATTTCTCTCATGAGT
1861 ---------+---------+---------+---------+---------+---------+ 1920
      K  C  P  I  C  R  G  T  I  K  G  T  V  R  T  F  L  S  *     -

     GAAGAATGGTCTGAAAGTATTGTTGGACATCAGAAGCTGTCAGAACAAAGAATGAACTAC
1921 ---------+---------+---------+---------+---------+---------+ 1980
     TGATTTCAGCTCTTCAGCAGGACATTCTACTCTCTTTCAAGATTAGTAATCTTGCTTTAT
1981 ---------+---------+---------+---------+---------+---------+ 2040
     GAAGGGTAGCATTGTATATTTAAGCTTAGTCTGTTGCAAGGGAAGGTCTATGCTGTTGAG
2041 ---------+---------+---------+---------+---------+---------+ 2100
     CTACAGGACTGTGTCTGTTCCAGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGA
2101 ---------+---------+---------+---------+---------+---------+ 2160
     CTTCTTGGGATTTGGGAATTTGGGGAAAGCTTTGGAATCCAGTGATGTGGAGCTCAGAAA
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TCCTGGAACCAGTGACTCTGGTACTCAGTAGATAGGGTACCCTGTACTTCTTGGTGCTTT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TCCAGTCTGGGAAATAAGGAGGAATCTGCTGCTGGTAAAAATTTGCTGGATGTGAGAAAT
2281 ---------+---------+---------+---------+---------+---------+ 2340
     AGATGAAAGTGTTTCGGGTGGGGGCGTGCATCAGTGTAGTGTGTGCAGGGATGTATGCAG
2341 ---------+---------+---------+---------+---------+---------+ 2400
     GCCAAACACTGTGTAG
2401 ---------+------ 2416
```

Fig. 6F

Alignment of BIR (Baculoviral IAP Repeats) Domains

Baculovirus

Cp_iap	Cydia pomonella
Op_iap	Orgyia pseudotsugata

Human

xiap	IAP on X chromosome
hiap1, hiap2	two different human IAP genes

Mouse

m-xiap	mouse homologue of human xiap gene

Insect

diap	Drosophilia IAP gene, not clearly a homologue of xiap or hiap

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.

Fig. 7

```
                                1                                                   68
SEQ ID NO:11   Op_iap-1    kaaRLgTYtn WPvqf.leps rMAasGFYYl GrgDeVrCaf CkveitnWvr gDdpetdHkr waPqCpFV
SEQ ID NO:14   Cp_iap-1    eevRLnTFek WPvsf.lspe tMAknGFYYl GrsDeVrCaf CkveimrWke gEdpaadHkk waPqCpFV
SEQ ID NO:15   diap-2      eanRLvTFkd WPnpn.iLpq aLAkAGFYYl nrlDhVkCvw CngviakWek nDnafeeHkr ffPqCprV
SEQ ID NO:16   m-xiap-1    efnRLkTFan FPssspvsas tLArAGFLYt GegDtVqCFs ChaaidrWqy gDsavgrHrr isPnCrFI
SEQ ID NO:17   xiap-1      efnRLkTFan FPsgspvsas tLArAGFLYt GegDtVrCFs ChaavdrWqy gDsavgrHrk vsPnCrFI
SEQ ID NO:18   hiap1-1     elyRMsTYst FPagvpvser sLArAGFYYt GvnDkVkCFc CglmldnWkr gDsptekHkk lyPsCrFV
SEQ ID NO:19   hiap2-1     elyRMsTYst FPagvpvser sLArAGFYYt GvnDkVkCFc CglmldnWkl gDspiqkHkq lyPsCsFI
SEQ ID NO:20   m-xiap-2    eeaRLksFqn WPdyahltpr eLAsAGLYYt GadDqVqCFc CggklknWep cDrawseHrr hfPnCfFv
SEQ ID NO:21   xiap-2      eeaRLksFqn WPdyahltpr eLAsAGLLYt GigDqVqCFc CggklknWep cDrawseHrr hfPnCfFV
SEQ ID NO:22   hiap1-2     enaRLlTFqt WP.lLflspt dLArAGFYYi GpgDrVaCFa CggklsnWep kDnamseHlr hfPkCpFI
SEQ ID NO:23   hiap2-2     eeaRFlTYhm WP.lLflsps eLArAGFYYi GpgDrVaCFa CggklsnWep kDdamseHrr hfPnCpFl
SEQ ID NO:24   m-xiap-3    yeaRivTFgt Wiysv..nke qLArAGFYal GegDkVkCFh CgggltdWkp sEdpwdqHak cyPgCkYl
SEQ ID NO:25   xiap-3      yeaRifTFgt Wiysv..nke qLArAGFYal GegDkVkCFh CgggltdWkp sEdpweqHak wyPgCkYl
SEQ ID NO:26   hiap1-3     haaRFkTFfn WPssvlvnpe qLAsAgFYYv GnsDdVkCFc CdgglrcWes gDdpwvqHak wfPrC Yl
SEQ ID NO:27   hiap2-3     haaRMrTFmy WPssvpvqpe qLAsAGFYYv GrnDdVkCFg CdgglrcWes gDdpwveHak wfPrCeFl
SEQ ID NO:28   Op_iap-2    eaaRLrTFae WPrglkqrpe eLAeAGFFYt GqgDktrCFc CdgglkdWep dDapwqqHar wydrCeYV
SEQ ID NO:29   Cp_iap-2    eaaRvksFhn WPrcmkqrpe qMAdAGFFYt GygDntkCFy CdgglkdWep eDvpweqHvr widrCaYV
SEQ ID NO:30   diap-3      vdaRLrTFtd WPisniqpas aLAqAGLYYq kigDqVrCFh CniglrsWqk eDepwieHak wsPkCqFV
SEQ ID NO:31   diap-1      esvRLaTFge WPlnapvsae dLvanGFF.. GtwmeaeCdf ChvridrWey gDlvaerHrr ssPiCsmV
SEQ ID NO:2    Consensus   ---RL-TF-- WP-------- -LA-AGFYY- G--D-V-CF- C------W-- -D-----H-- --P-C-FV
```

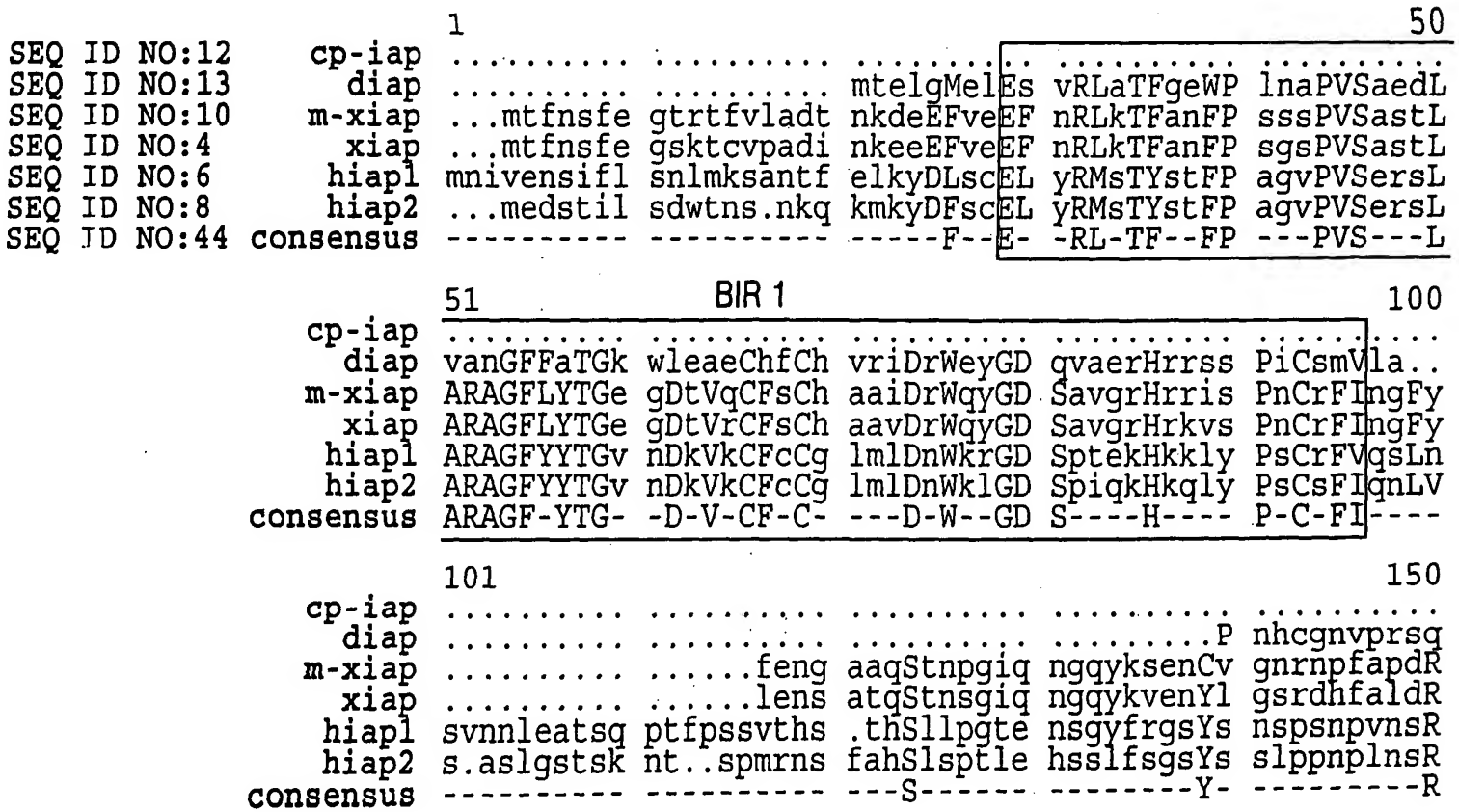
1
50
SEQ ID NO:12 cp-iap
SEQ ID NO:13 diap
SEQ ID NO:10 m-xiap
SEQ ID NO:4 xiap
SEQ ID NO:6 hiap1
SEQ ID NO:8 hiap2
SEQ ID NO:44 consensus
mtelgMelEs vRLaTFgeWP lnaPVSaedL
...mtfnsfe gtrtfvladt nkdeEFveEF nRLkTFanFP sssPVSastL
...mtfnsfe gsktcvpadi nkeeEFveEF nRLkTFanFP sgsPVSastL
mnivensifl snlmksantf elkyDLscEL yRMsTYstFP agvPVSersL
...medstil sdwtns.nkq kmkyDFscEL yRMsTYstFP agvPVSersL
51
BIR 1
100
cp-iap
diap
m-xiap
xiap
hiap1
hiap2
consensus
vanGFFaTGk wleaeChfCh vriDrWeyGD qvaerHrrss PiCsmVla..
ARAGFLYTGe gDtVqCFsCh aaiDrWqyGD SavgrHrris PnCrFIngFy
ARAGFLYTGe gDtVrCFsCh aavDrWqyGD SavgrHrkvs PnCrFIngFy
ARAGFYYTGv nDkVkCFcCg lmlDnWkrGD SptekHkkly PsCrFVqsLn
ARAGFYYTGv nDkVkCFcCg lmlDnWklGD SpiqkHkqly PsCsFIqnLV
ARAGF-YTG- -D-V-CF-C- ---D-W--GD S----H---- P-C-FI----
101
150
cp-iap
diap
m-xiap
xiap
hiap1
hiap2
consensus
.....feng aaqStnpgiq ngqyksenCv gnrnpfapdR
.....lens atqStnsgiq ngqykvenYl gsrdhfaldR
svnnleatsq ptfpssvths .thSllpgte nsgyfrgsYs nspsnpvnsR
s.aslgstsk nt..spmrns fahSlsptle hsslfsgsYs slppnplnsR
---S------ -------Y- ---------R

Fig. 8A

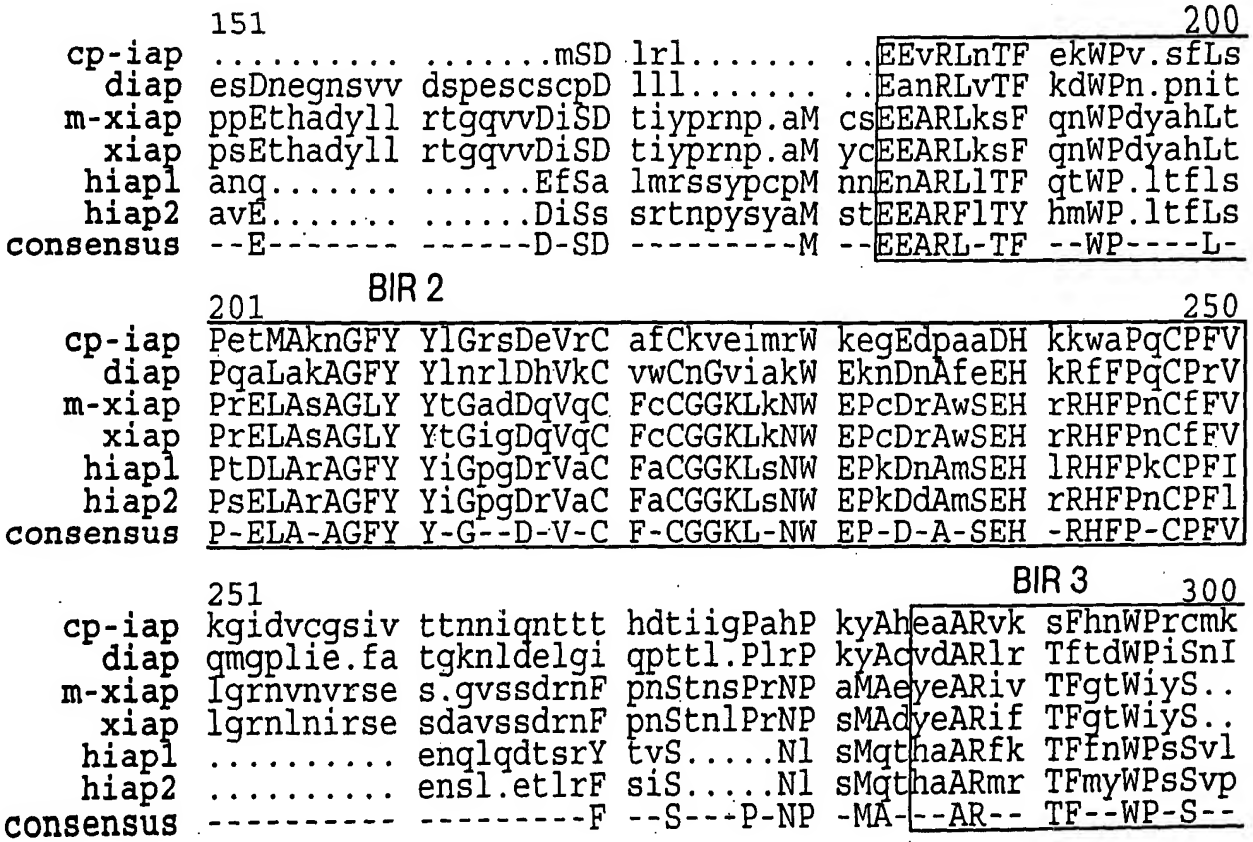
151
200
cp-iap ....mSD lrl..... ..EEvRLnTF ekWPv.sfLs
diap esDnegnsvv dspescscpD lll..... ..EanRLvTF kdWPn.pnit
m-xiap ppEthadyll rtgqvvDiSD tiyprnp.aM csEEARLksF qnWPdyahLt
xiap psEthadyll rtgqvvDiSD tiyprnp.aM ycEEARLksF qnWPdyahLt
hiap1 anq..... .....EfSa lmrssypcpM nnEnARL1TF qtWP.1tfls
hiap2 avE..... .....DiSs srtnpysyaM stEEARF1TY hmWP.1tfLs
consensus --E------- ------D-SD ---------M --EEARL-TF --WP----L-
BIR 2
201
250
cp-iap PetMAknGFY YlGrsDeVrC afCkveimrW kegEdpaaDH kkwaPqCPFV
diap PqaLakAGFY Ylnr1DhVkC vwCnGviakW EknDnAfeEH kRfFPqCPrV
m-xiap PrELAsAGLY YtGadDqVqC FcCGGKLkNW EPcDrAwSEH rRHFPnCfFV
xiap PrELAsAGLY YtGigDqVqC FcCGGKLkNW EPcDrAwSEH rRHFPnCfFV
hiap1 PtDLArAGFY YiGpgDrVaC FaCGGKLsNW EPkDnAmSEH 1RHFPkCPFI
hiap2 PsELArAGFY YiGpgDrVaC FaCGGKLsNW EPkDdAmSEH rRHFPnCPF1
consensus P-ELA-AGFY Y-G--D-V-C F-CGGKL-NW EP-D-A-SEH -RHFP-CPFV
BIR 3
251
300
cp-iap kgidvcgsiv ttnniqnttt hdtiigPahP kyAheaARvk sFhnWPrcmk
diap qmgplie.fa tgknldelgi qpttl.PlrP kyAcvdARlr TftdWPiSnI
m-xiap lgrnvnvrse s.gvssdrnF pnStnsPrNP aMAeyeARiv TFgtWiyS..
xiap lgrnlnirse sdavssdrnF pnStn1PrNP sMAdyeARif TFgtWiyS..
hiap1 ..... enqlqdtsrY tvS.....N1 sMqthaARfk TFfnWPsSv1
hiap2 ..... ensl.etlrF siS.....N1 sMqthaARmr TFmyWPsSvp
consensus ---------- ---------F --S---P-NP -MA---AR-- TF--WP-S--

Fig. 8B

BIR 3

```
           301                                                        350
cp-iap     qrpEQMAdAG FFYtGyGDnt KCFyCdGGLk dWepeDvPWe QHvrWFdrCa
  diap     qpasaLAqAG LYYqkiGdqv rCFhCniGLr sWqkeDEPWf eHAKWsPkCq
m-xiap     VnkEQLArAG FYalGeGDkV KCFhCgGGLt dWkpsEDPWd QHAKcYPgCk
  xiap     VnkEQLArAG FYalGeGDkV KCFhCgGGLt dWkpsEDPWd QHAKWYPgCk
 hiap1     VnpEQLAsAG FYYvGnsDdV KCFcCdGGLr cWesgDDPWv QHAKWFPrCe
 hiap2     VqpEQLAsAG FYYvGRsDdV KCFgCdGGLr cWesgDDPWv eHAKWFPrCe
consensus  V--EQLA-AG FYY-G-GD-V KCF-C-GGL- -W---DDPW- QHAKWFP-C-

           351                                                        400
cp-iap     YvqlvKGrDY VqkVit.... .......... ....e..... ..........
  diap     FvllaKGpaY VseVlattaa nassqpaTap aptlq..... ..........
m-xiap     YLldeKGQEY InnIhlthp. LeEsLgrTae kt........ .....Ppltk
  xiap     YLleqKGQEY InnIhlths. LeEcLvrTte kt........ .....Psltr
 hiap1     YLiriKGQEY IrqVqasyph LlEqLlsTsD spgdenaess iihlePgedh
 hiap2     FLirmKGQEF VdeIqgryph LlEqLlsTsD ttgeenadpp iihfgPgess
consensus  YL---KGQEY ---------- L-E-L--T-- ---------- -----P----

           401                                                        450
cp-iap     ..acVLpge. .......... .......... .......... ..........
  diap     ..adVLmdea pakeAltLGi dggvVrnaiq rKllssGcaF stldeLlhDi
m-xiap     kiDdtifqnP mVqeAirMGF sfkdlKktme eKIqtsGssY lslevLIaDL
  xiap     riDdtifqnP mVqeAirMGF sfkdIKkime eKIqisGsnY kslevLVaDL
 hiap1     seDaIMmntP vInaAveMGF srslVKqtvq rKIlatGenY rlvndLVlDL
 hiap2     seDaVMmntP vVksAleMGF nrdlVKqtvl sKIlttGenY ktvndiVsaL
consensus  --D-V----P -V--A--MGF ----VK---- -KI---G--Y -----LV-DL
```

Fig. 8C

```
           451                                                        500
cp-iap     .......... .......... .......... .......... ..........
  diap     fddagagaal Evreppe...  .......... .......... ..........
m-xiap     vsAqkDnteD E.......... .......... .......... ..........
  xiap     vnAqkDsmqD E.......... .......... .......... ..........
 hiap1     lnAedEireE Ererateeke sndlllirkn rmalfqhltc vipildslLt
 hiap2     lnAedEkreE Ekekqaeema sddlslirkn rmalfqqltc vlpildnllk
consensus  --A------- E--------- ---------- ---------- ----------

           501                                                        550
cp-iap     .......... .......... ..nttvstaa pvsepipe.. ..........
  diap     .......... ...psapfie pcqattskaa svpipvadsi pakpqaaeav
m-xiap     .......... ....ssQtsL Q.......... .......... ..........
  xiap     .......... ....ssQtsL Q.......... .......... ..........
 hiap1     agiineqehd vikqktQtsL Qarelidtil vkgniaatvf rnslqeaeav
 hiap2     anvinkqehd iikqktQipL Qarelidtiw vkgnaaanif knclkeidst
consensus  ---------- ------Q--L Q--------- ---------- ----------
```

Fig. 8D

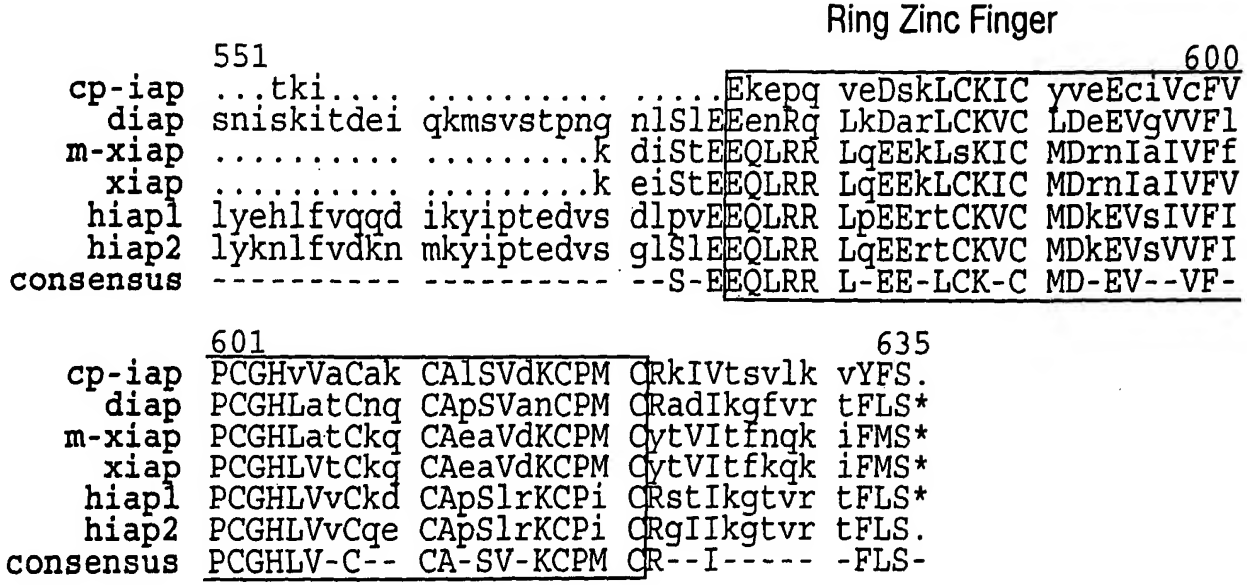
Ring Zinc Finger
551
600
cp-iap ...tki.... ....Ekepq veDskLCKIC yveEciVcFV
diap sniskitdei qkmsvstpng nlSlEEenRq LkDarLCKVC LDeEVgVVFl
m-xiap ....k diStEEQLRR LqEEkLsKIC MDrnIaIVFf
xiap ....k eiStEEQLRR LqEEkLCKIC MDrnIaIVFV
hiap1 lyehlfvqqd ikyiptedvs dlpvEEQLRR LpEErtCKVC MDkEVsIVFI
hiap2 lyknlfvdkn mkyiptedvs glSlEEQLRR LqEErtCKVC MDkEVsVVFI
consensus ---------- ---------- --S-EEQLRR L-EE-LCK-C MD-EV--VF-
601
635
cp-iap PCGHvVaCak CAlSVdKCPM CRkIVtsvlk vYFS.
diap PCGHLatCnq CApSVanCPM CRadIkgfvr tFLS*
m-xiap PCGHLatCkq CAeaVdKCPM CytVItfnqk iFMS*
xiap PCGHLVtCkq CAeaVdKCPM CytVItfkqk iFMS*
hiap1 PCGHLVvCkd CApSlrKCPi CRstIkgtvr tFLS*
hiap2 PCGHLVvCqe CApSlrKCPi CRgIIkgtvr tFLS.
consensus PCGHLV-C-- CA-SV-KCPM CR--I----- -FLS-

Fig. 8E

Alignment of RZF (Ring Zinc Finger) Domains

Baculovirus	
Cp_iap	Cydia pomonella
Op_iap	Orgyia pseudotsugata
Human	
xiap	IAP on X chromosome
hiap1, hiap2	two different human IAP genes
Mouse	
m-xiap	mouse homologue of human xiap gene
Insect	
diap	Drosophilia IAP gene, not clearly a homologue of xiap or hiap

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

```
                          1                                                46
SEQ ID NO:32 hiap2        EqlrrlqEer tCKVCMdkev sVvFiPCGHl vvCqeCApel rkCPiC
SEQ ID NO:33 hiap1        EqlrrlpEer tCKVCMdkev sIvFiPCGHl w CkdCApsl rkCPiC
SEQ ID NO:34 m-xiap       EqlrrlqEek lsKICMdrni aIvFfPCGHl atCkqCAeav dkCPmC
SEQ ID NO:35 xiap         EqlrrlqEek lCKICMdrni aIvFvPCGHl vtCkqCAeav dkCPmC
SEQ ID NO:36 diap         EenrqlkDar lCKVCLdeev gVvFlPCGHl atCnqCApev anCPmC
SEQ ID NO:37 Cp_iap       EkepgveDsk lCKICyveec iVcFvPCGHv vaCakCAlsv dkCPmC
SEQ ID NO:38 Op_iap       aveaevaDdr lCKICLgack tVcFvPCGHv vaCgkCAagv ttCPvC
SEQ ID NO:1  consensus    E------E-- -CKICM---- -V-F-PCGH- --C--CA--- --CP-C
```

Fig. 9

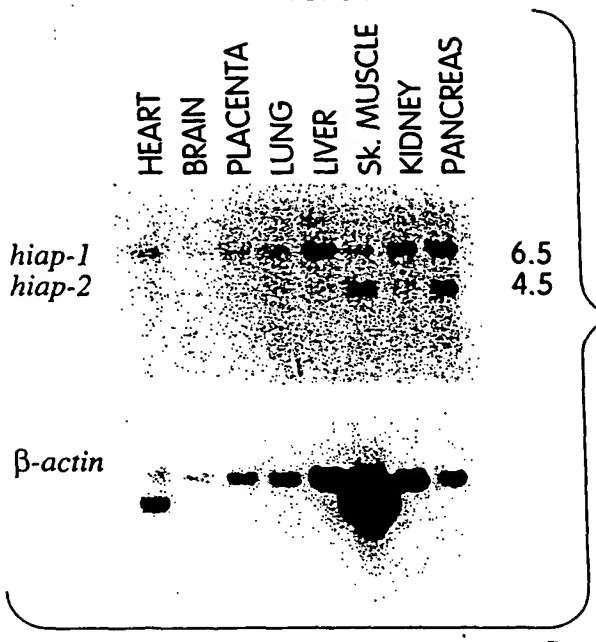

Fig. 10A

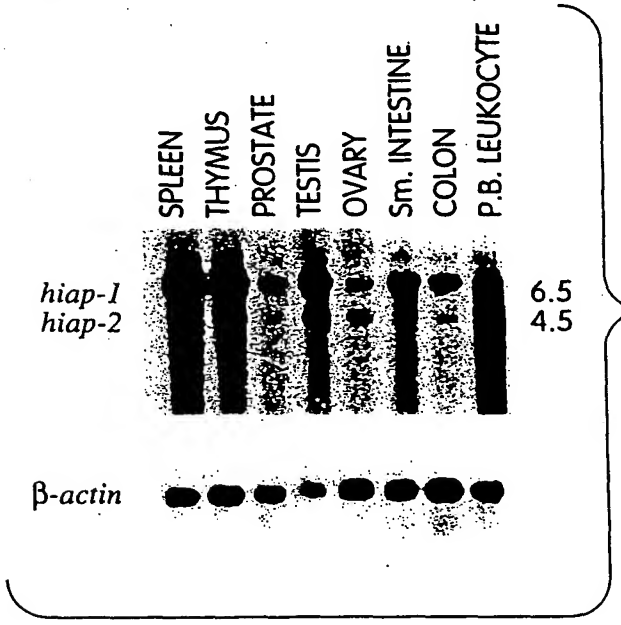

Fig. 10B

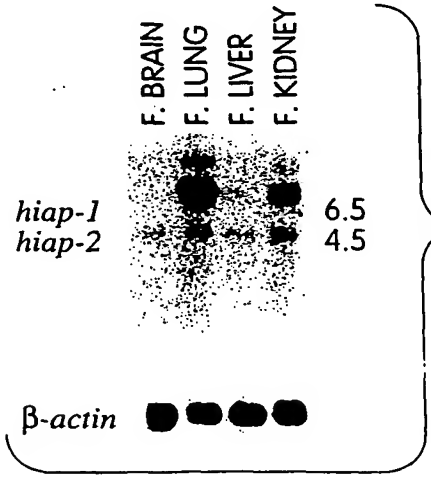

Fig. 10C

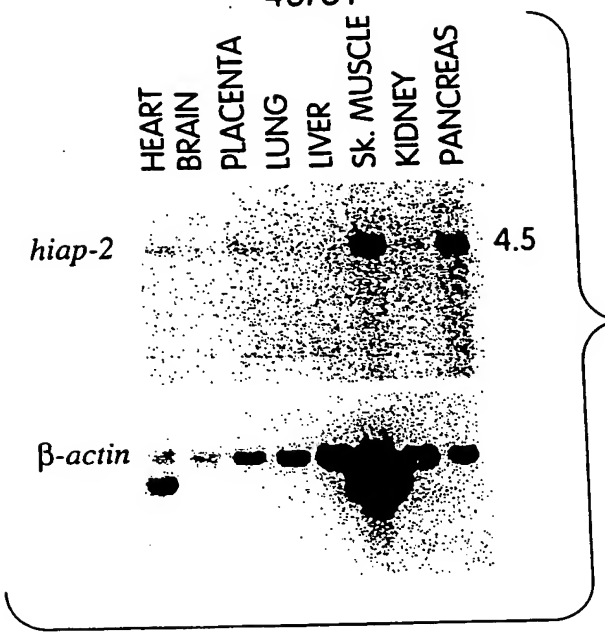

Fig. 11A

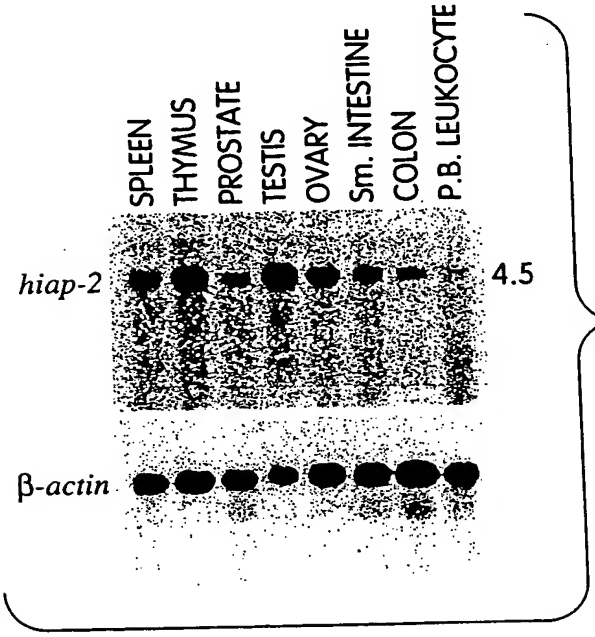

Fig. 11B

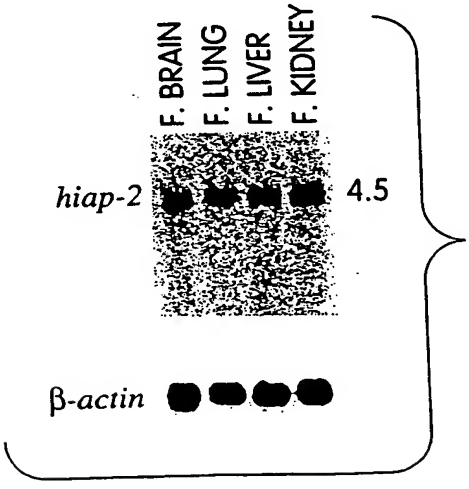

Fig. 11C

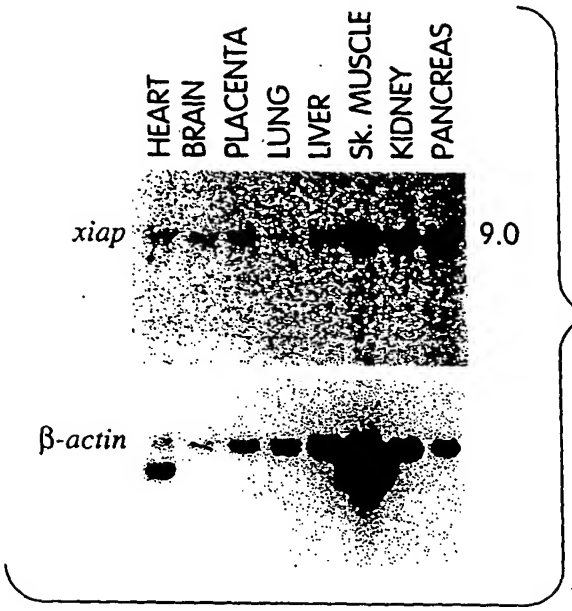

Fig. 12A

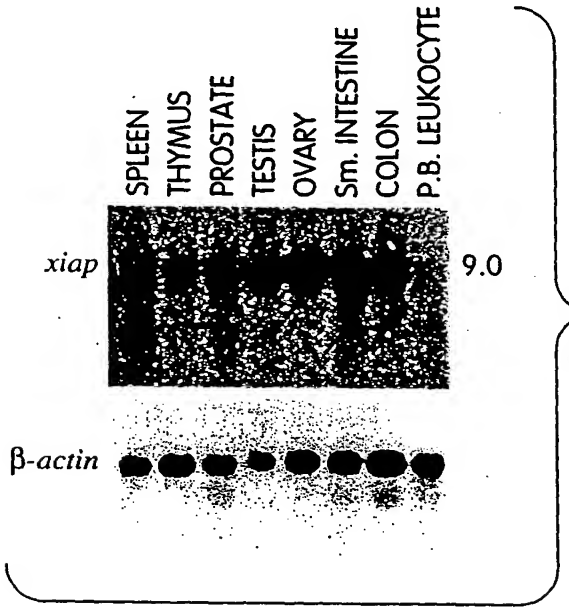

Fig. 12B

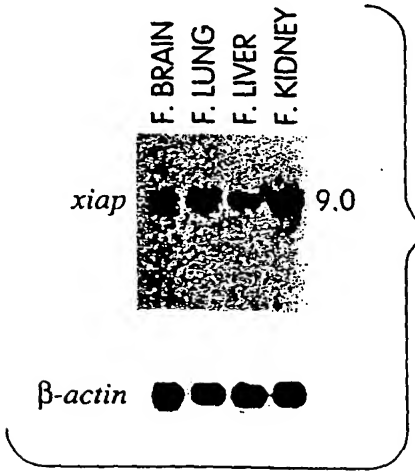

Fig. 12C

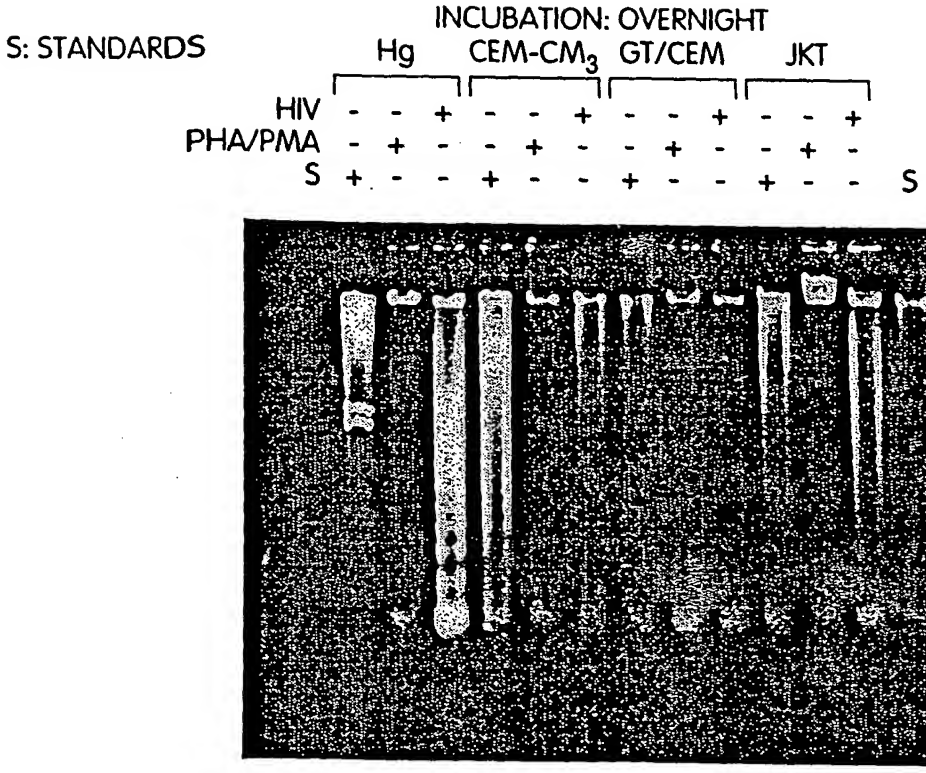

Fig. 13A

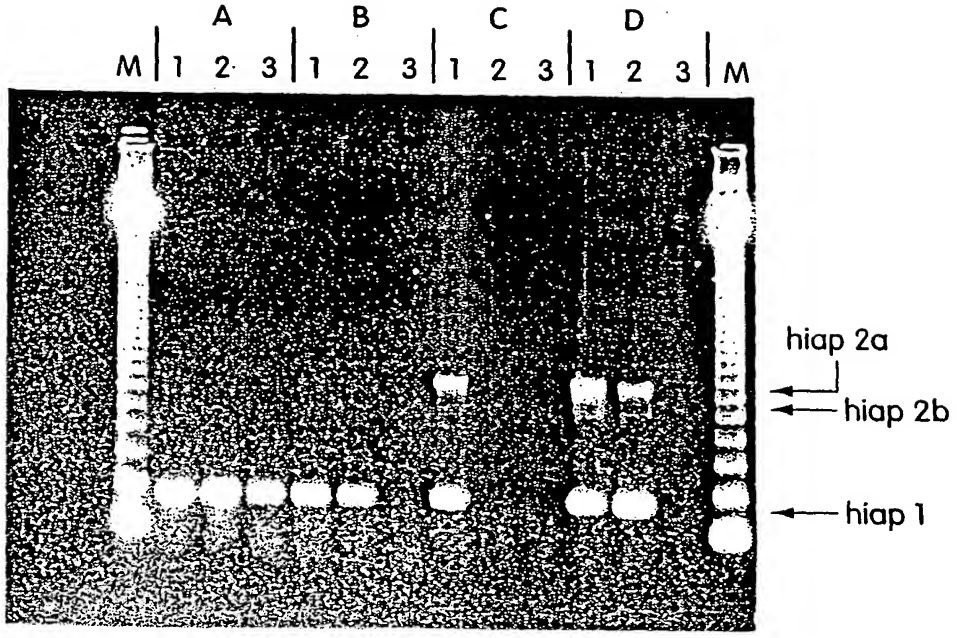

Fig. 13B

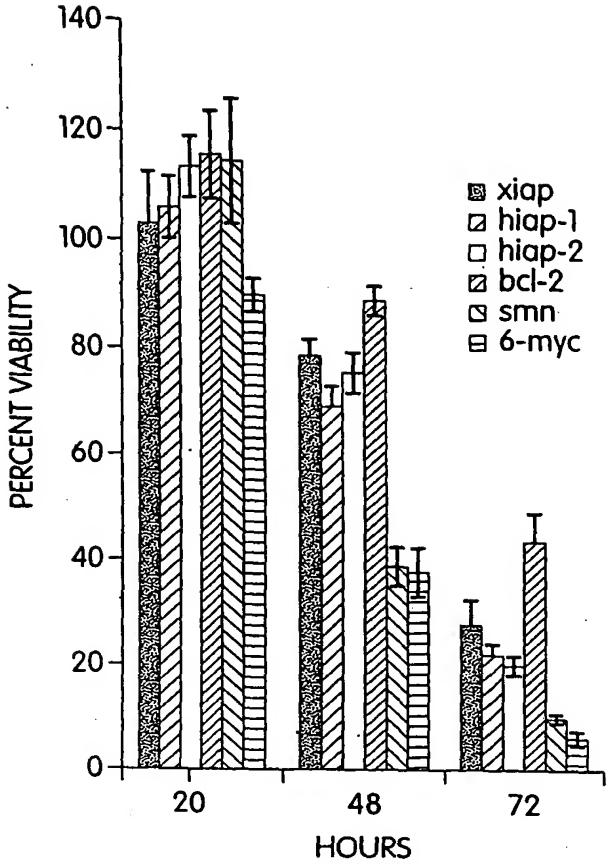

Fig. 14A

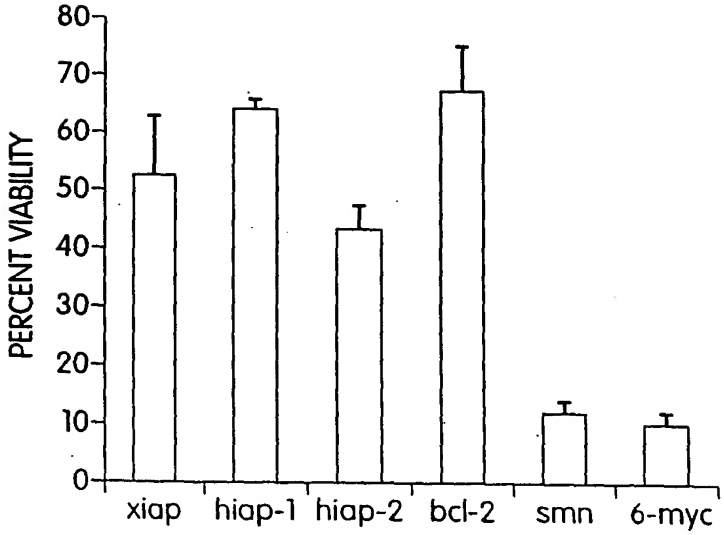

Fig. 14B

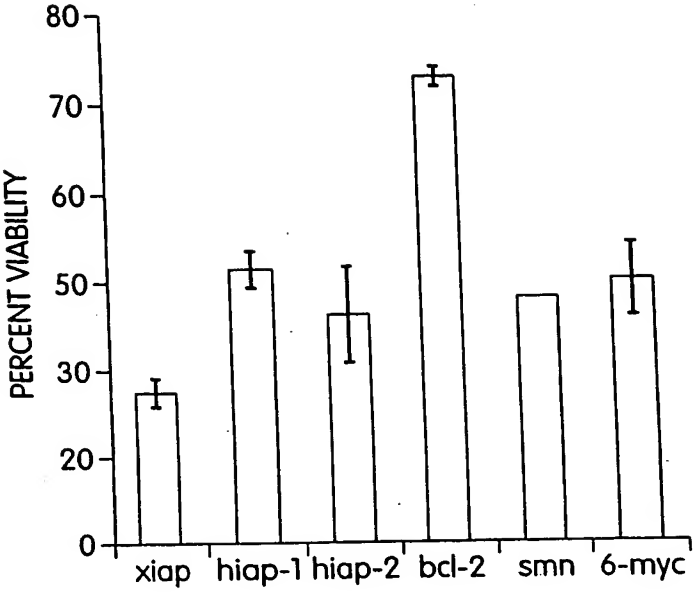

Fig. 14C

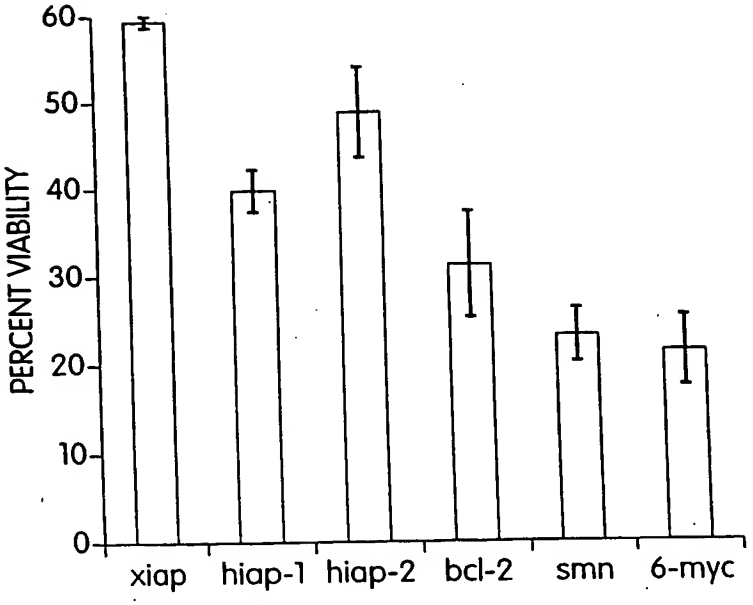

Fig. 14D

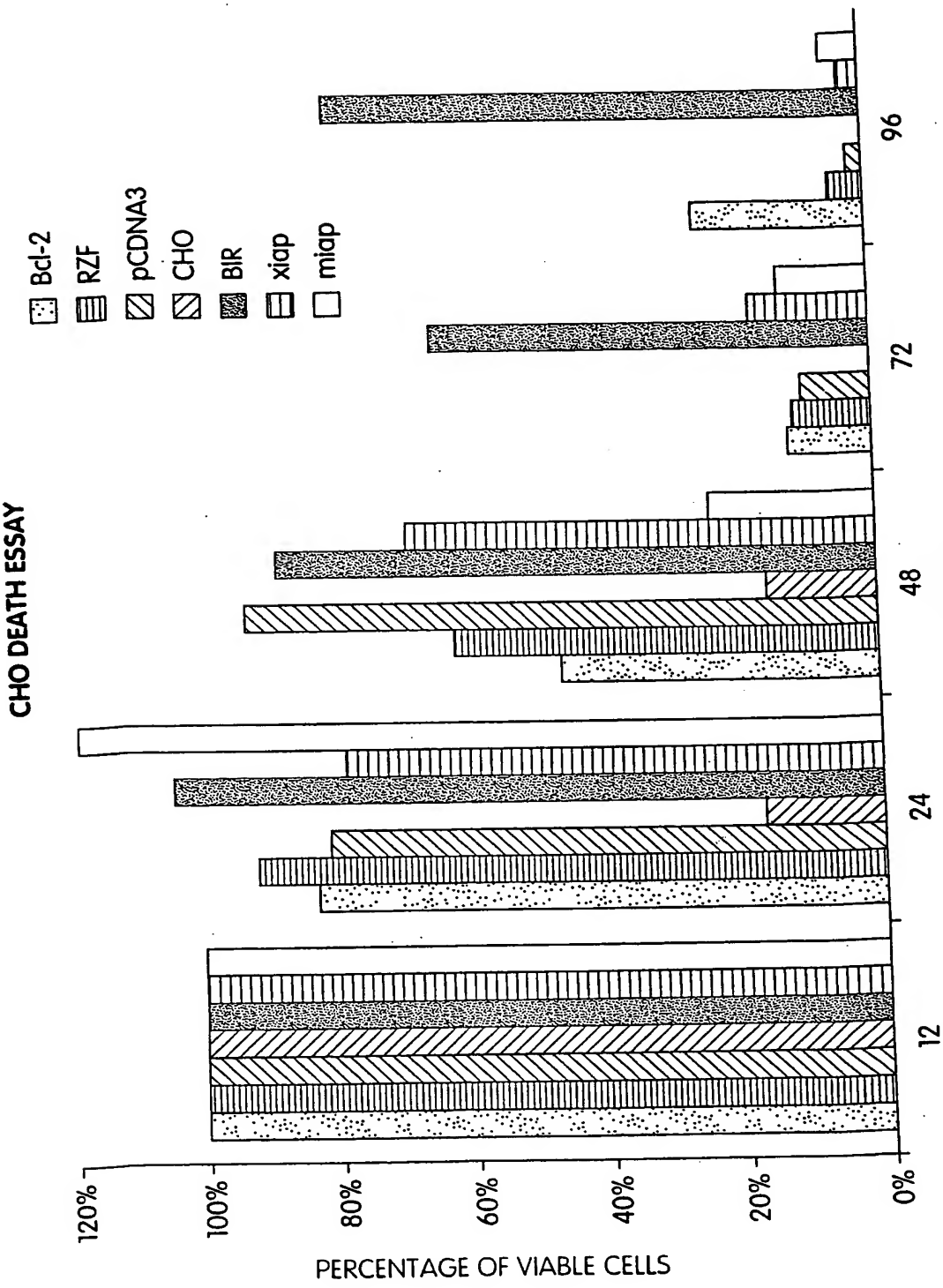
CHO DEATH ESSAY
Bcl-2
RZF
pCDNA3
CHO
BIR
xiap
miap
120%
100%
80%
60%
40%
20%
0%
PERCENTAGE OF VIABLE CELLS
12
24
48
72
96
HOURS

Fig. 15A

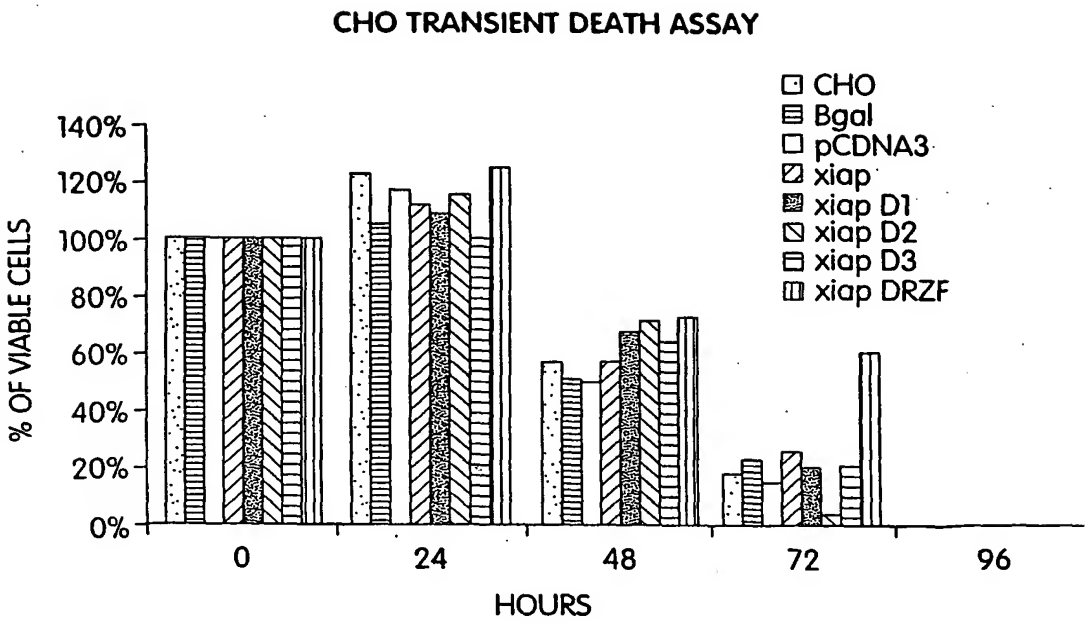
CHO TRANSIENT DEATH ASSAY
CHO
Bgal
pCDNA3
xiap
xiap D1
xiap D2
xiap D3
xiap DRZF
140%
120%
100%
80%
60%
40%
20%
0%
% OF VIABLE CELLS
0
24
48
72
96
HOURS

Fig. 15B

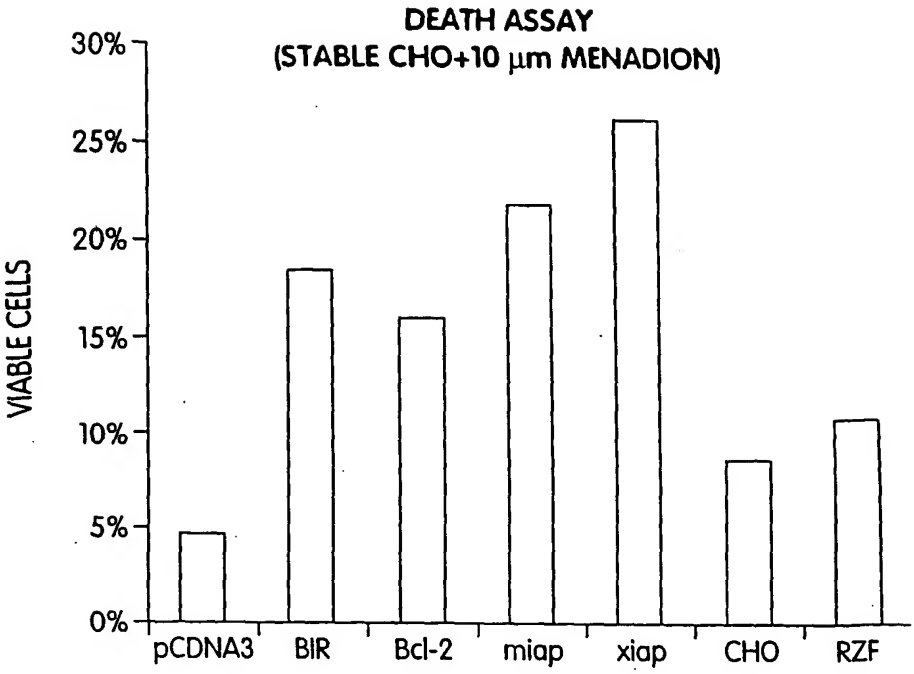

Fig. 16A

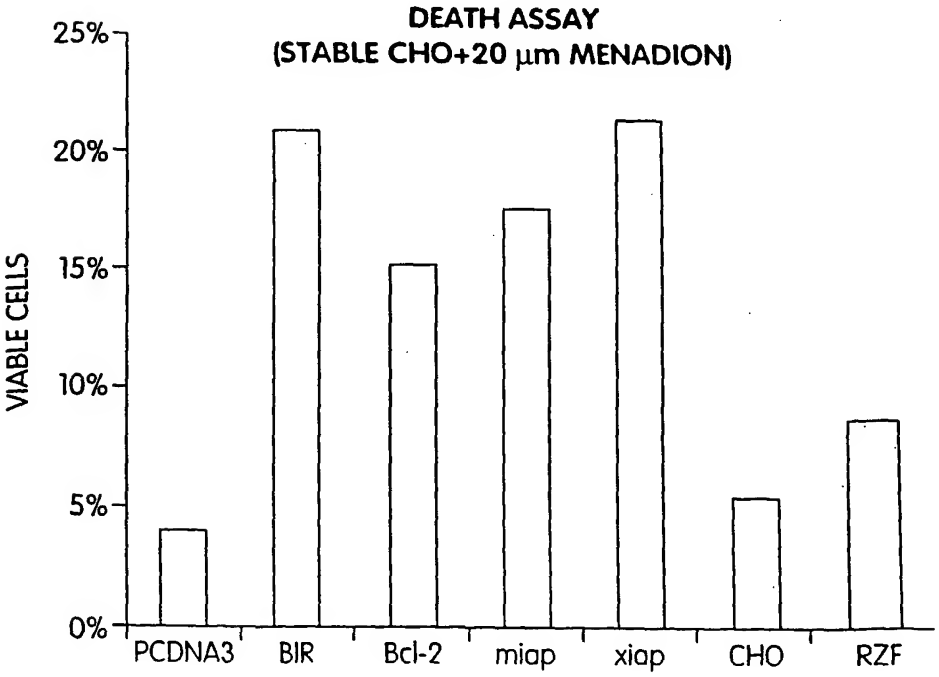

Fig. 16B

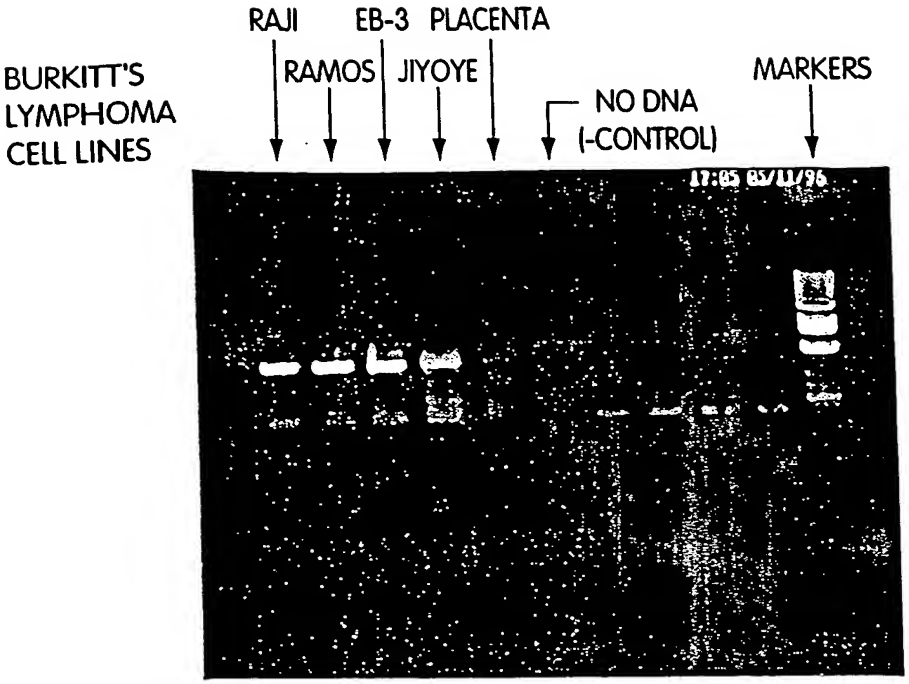
BURKITT'S
LYMPHOMA
CELL LINES
RAJI
RAMOS
EB-3
JIYOYE
PLACENTA
NO DNA
(-CONTROL)
MARKERS

Fig. 17

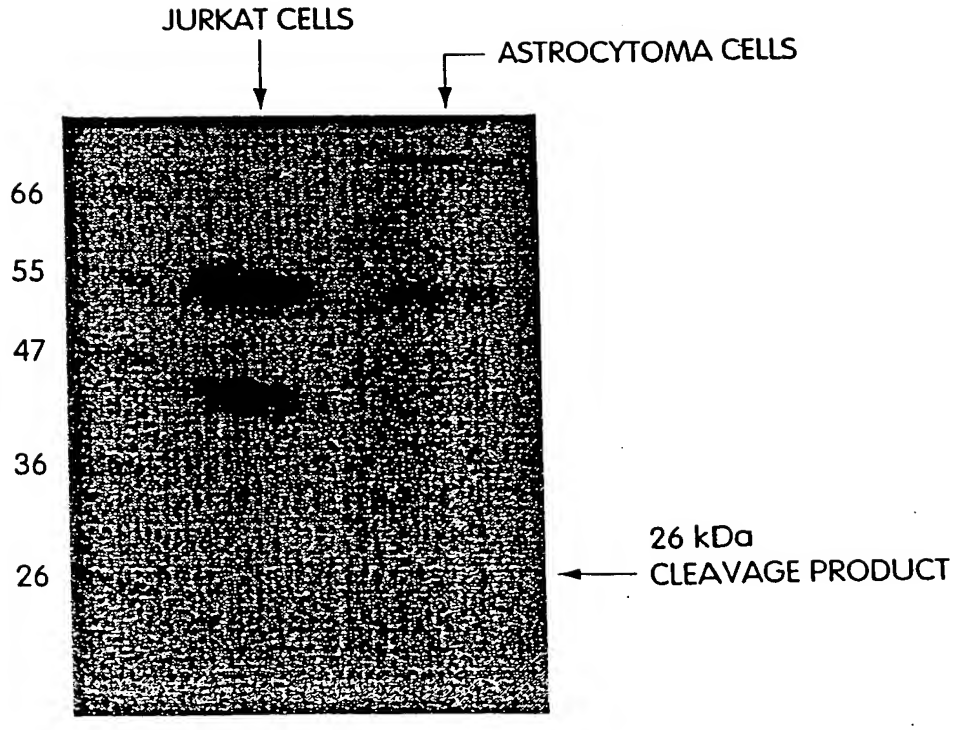
JURKAT CELLS
ASTROCYTOMA CELLS
66
55
47
36
26
26 kDa
CLEAVAGE PRODUCT

Fig. 18

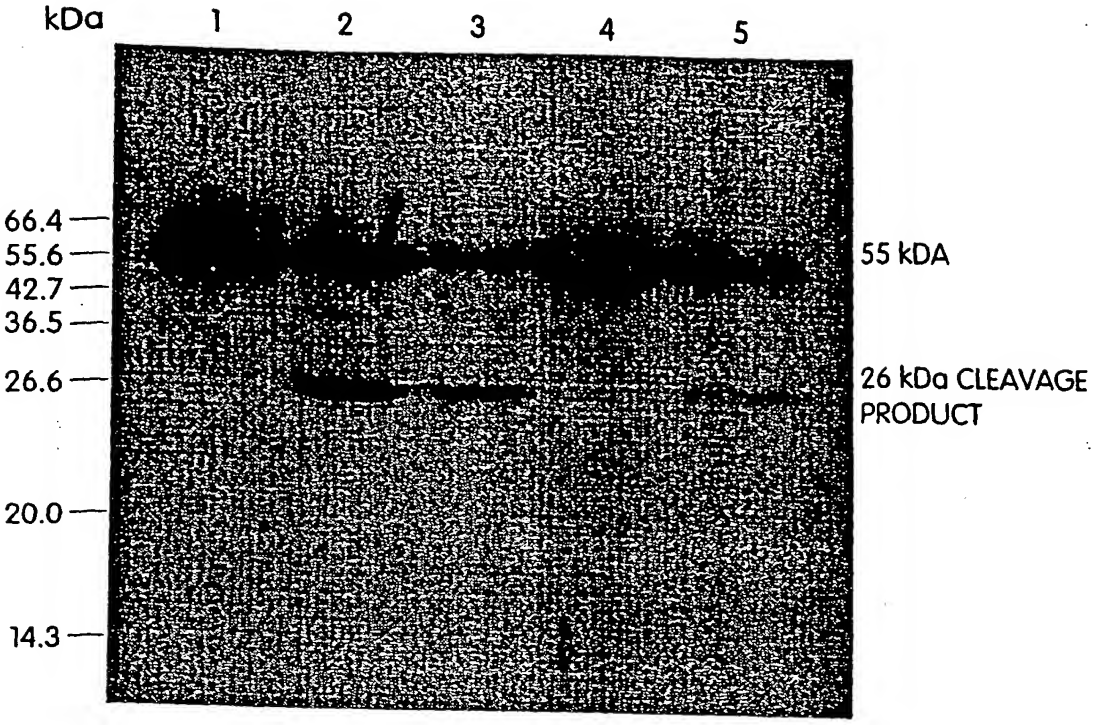
kDa
1
2
3
4
5
66.4
55.6
42.7
36.5
26.6
20.0
14.3
55 kDA
26 kDa CLEAVAGE PRODUCT

Fig. 19

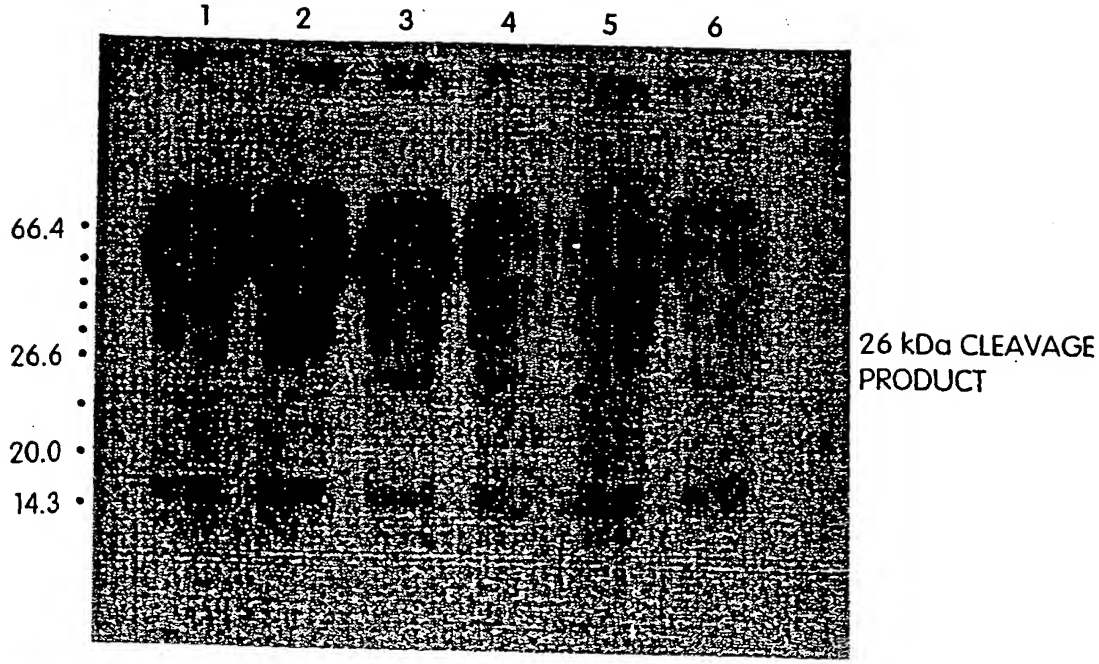
1
2
3
4
5
6
66.4
26.6
20.0
14.3
26 kDa CLEAVAGE PRODUCT

Fig. 20

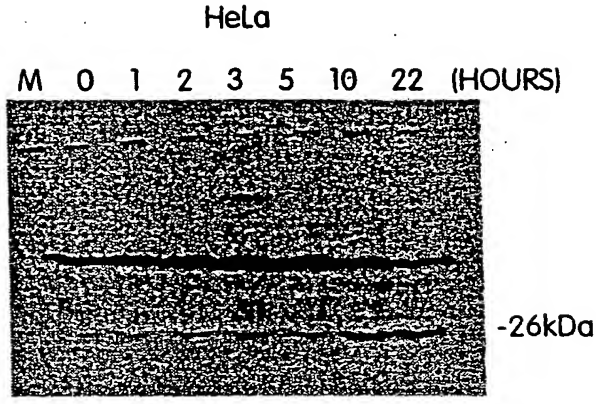

Fig. 21A

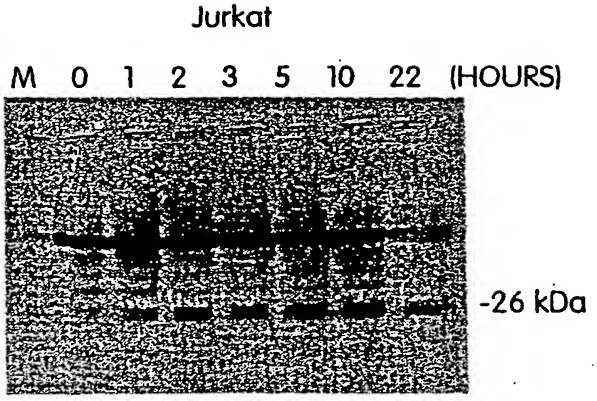

Fig. 21B

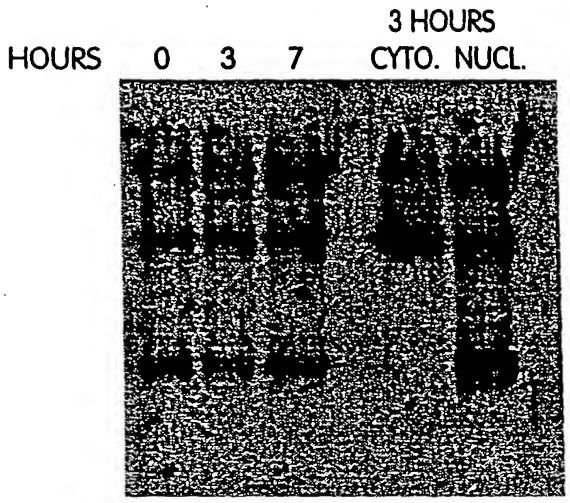

Fig. 22A

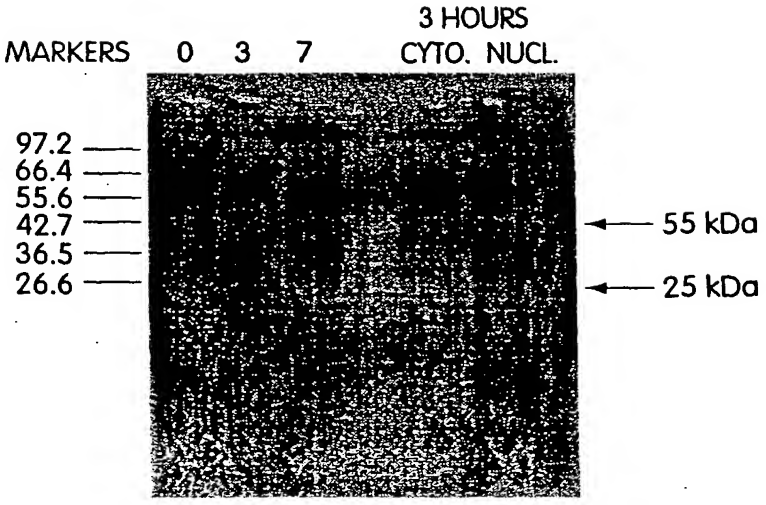

Fig. 22B

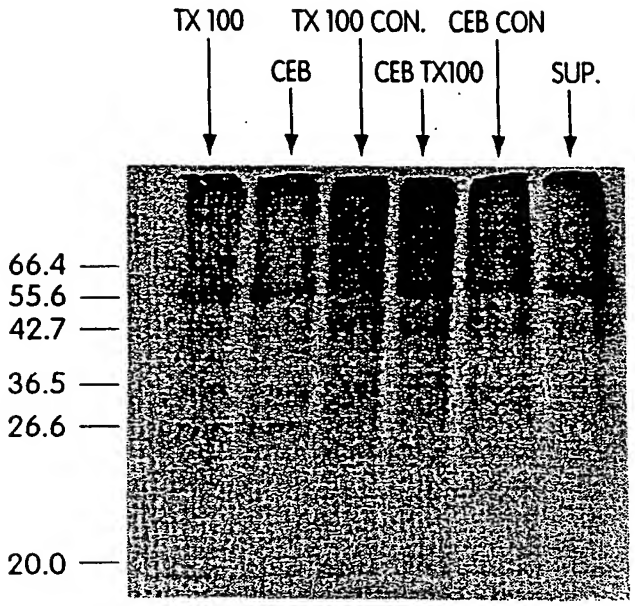
TX 100
TX 100 CON.
CEB CON
CEB
CEB TX100
SUP.
66.4
55.6
42.7
36.5
26.6
20.0

Fig. 23